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OM protein - protein search, using sw model

Run on:   May 4, 2005, 22:04:58 ; Search time 172 Seconds
                                   (without alignments)
                                   1668.466 Million cell updates/sec

Title:        US-10-090-215-12
Perfect score: 3858
Sequence:     1 MADSSEGPRAGPGEVAELPG.........GQVSKESKHIWKLQSGRRRL 742
Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5
Searched:     2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:      2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_Geneseq_16Dec04:*
         1: geneseqp1980s:*
         2: geneseqp1990s:*
         3: geneseqp2000s:*
         4: geneseqp2001s:*
         5: geneseqp2002s:*
         6: geneseqp2003as:*
         7: geneseqp2003bs:*
         8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3858 | 100.0 | 742 | 4 | AAE06683 | Aae06683 Human van |
| 2 | 3829 | 99.2 | 831 | 8 | ADI81606 | Adi81606 Human van |
| 3 | 3829 | 99.2 | 871 | 4 | AAE01227 | Aae01227 Human van |
| 4 | 3829 | 99.2 | 871 | 5 | AAG65787 | Aag65787 Human ion |
| 5 | 3829 | 99.2 | 871 | 5 | AAU74935 | Aau74935 Amino aci |
| 6 | 3829 | 99.2 | 871 | 5 | ABB79191 | Abb79191 Human VR4 |
| 7 | 3829 | 99.2 | 871 | 5 | ADG64947 | Adg64947 VANILREP4 |
| 8 | 3829 | 99.2 | 871 | 7 | ADG32562 | Adg32562 Human TRP |
| 9 | 3829 | 99.2 | 871 | 7 | ADL71047 | Adl71047 Type II c |
| 10 | 3829 | 99.2 | 871 | 8 | ADI81584 | Adi81584 Human van |
| 11 | 3829 | 99.2 | 871 | 8 | ADI81608 | Adi81608 Human OTR |
| 12 | 3829 | 99.2 | 871 | 8 | ADI81588 | Adi81588 Human van |
| 13 | 3828 | 99.2 | 871 | 5 | ABB98197 | Abb98197 Human VR- |
| 14 | 3828 | 99.2 | 871 | 8 | ADI81590 | Adi81590 Human van |
| 15 | 3828 | 99.2 | 970 | 7 | ADE08372 | Ade08372 Novel pro |
| 16 | 3825 | 99.1 | 871 | 5 | ABB98198 | Abb98198 Human VR- |
| 17 | 3823 | 99.1 | 871 | 8 | AAE06681 | Aae06681 Human van |
| 18 | 3810 | 98.8 | 963 | 3 | AAY96479 | Aay96479 Human van |
| 19 | 3810 | 98.8 | 963 | 5 | AAU95381 | Aau95381 Human cal |
| 20 | 3809 | 98.7 | 871 | 4 | AAG67210 | Aag67210 Amino aci |
| 21 | 3777.5 | 97.9 | 1051 | 7 | ADE08373 | Ade08373 Novel pro |
| 22 | 3695 | 95.8 | 871 | 7 | ADL71045 | Adl71045 Type II c |
| 23 | 3695 | 95.8 | 871 | 8 | ADI81614 | Adi81614 Mouse tra |
| 24 | 3693 | 95.7 | 871 | 8 | ADI81596 | Adi81596 Rat vanil |
| 25 | 3689 | 95.6 | 871 | 4 | AAB86980 | Aab86980 Murine OT |
| 26 | 3689 | 95.6 | 871 | 8 | ADI81610 | Adi81610 Mouse OTR |
| 27 | 3685 | 95.5 | 871 | 7 | ADG32559 | Adg32559 Murine TR |
| 28 | 3681 | 95.4 | 871 | 4 | AAG67209 | Aag67209 Amino aci |
| 29 | 3636 | 94.2 | 873 | 8 | ADI81594 | Adi81594 Mouse van |
| 30 | 3472 | 90.0 | 803 | 8 | ADI81586 | Adi81586 Human van |
| 31 | 3470 | 89.9 | 811 | 4 | AAE06682 | Aae06682 Human van |
| 32 | 3467 | 89.9 | 803 | 4 | AAG63208 | Aag63208 Amino aci |
| 33 | 3389 | 87.8 | 803 | 8 | ADI81592 | Adi81592 Mouse van |
| 34 | 3284 | 85.1 | 852 | 8 | ADI81566 | Adi81566 Chicken v |
| 35 | 3120 | 80.9 | 743 | 4 | AAG63209 | Aag63209 Amino aci |
| 36 | 2373.5 | 61.5 | 602 | 5 | AAU74936 | Aau74936 Amino aci |
| 37 | 2315.5 | 60.0 | 1115 | 4 | ABG28242 | Abg28242 Novel hum |
| 38 | 2156.5 | 55.9 | 559 | 5 | AAB16773 | Aab16773 Human tra |
| 39 | 1808 | 46.9 | 498 | 4 | AAE04889 | Aae04889 Human tra |
| 40 | 1604.5 | 41.6 | 843 | 2 | AAY06561 | Aay06561 Chicken c |
| 41 | 1601.5 | 41.5 | 843 | 2 | AAW99799 | Aaw99799 Chicken V |
| 42 | 1580.5 | 41.0 | 838 | 8 | ADI81568 | Adi81568 Rat vanil |
| 43 | 1579.5 | 40.9 | 838 | 2 | AAY06555 | Aay06555 Rat capsa |
| 44 | 1579.5 | 40.9 | 838 | 2 | AAW99789 | Aaw99789 Rat VR1 c |
| 45 | 1579.5 | 40.9 | 838 | 4 | AAE01228 | Aae01228 Rattus va |

ALIGNMENTS

```
RESULT 1
AAE06683
ID   AAE06683 standard; protein; 742 AA.
XX
AC   AAE06683;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human vanilloid receptor VR3 isoform, VR3A+B+.
XX
KW   Human; vanilloid receptor; VR3; inflammatory condition; analgesic;
KW   intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;
KW   postmastectomy pain; complex regional pain syndrome; arthritis;
KW   rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;
KW   chronic obstructive pulmonary disease; irritable bowel syndrome;
KW   psoriasis; central nervous system disease; CNS; cancer;
KW   intestinal tract disorder; VR3A+B+.
XX
OS   Homo sapiens.
XX
PN   WO200158945-A1.
XX
PD   16-AUG-2001.
XX
PF   01-FEB-2001; 2001WO-US003456.
XX
PR   08-FEB-2000; 2000US-00500123.
XX
PA   (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
PI   Dubin AE,  Huvar A,  Glass CA,   Erlander MG;
XX
DR   WPI; 2001-488969/53.
DR   N-PSDB; AAD12793.
XX
PT   New human VR3 receptor useful for the treatment of disorders including
PT   cancers arthritis and pain.
XX
PS   Claim 11; Fig 8; 104pp; English.
XX
CC   The patent relates to human vanilloid receptor VR3 polynucleotide and
CC   polypeptide. Three isoforms of VR3 namely VR3A-B-, VR3A-B- and VR3A+B+
CC   have also been disclosed. The VR3 polypeptide is used to identify its
CC   modulators which are useful for the treatment of inflammatory conditions
CC   and for use as analgesics for intractable pain associated with
CC   postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex
CC   regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis),
CC   as well as ulcers, neurodegenerative diseases, asthma, chronic
```

CC   obstructive pulmonary disease, irritable bowel syndrome and psoriasis.
CC   The VR3 modulators are also useful for treatment of central nervous
CC   system (CNS) diseases, diseases of the intestinal tract, abnormal
CC   proliferation and cancer. The present sequence is human VR3 receptor
CC   isoform, VR3A+B+
XX
SQ   Sequence 742 AA;

Query Match             100.0%;  Score 3858;  DB 4;  Length 742;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches   742;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
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Qy    241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
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Qy    301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
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Qy    361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
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Qy    421 LSSLDTCGEBASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
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Qy    661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
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Db    721 TVGQVSKESKHIWKLQSGRRRL 742
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RESULT 2
ADI81606
ID   ADI81606 standard; protein; 831 AA.
XX
AC   ADI81606;
XX
DT   22-APR-2004 (first entry)
XX

DE   Human vanilloid receptor-related channel protein #2.
XX
KW   Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
KW   neurological disease; inflammatory disease; cancer; Alzheimer's disease;
KW   Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
KW   hepatitis; cirrhosis; kidney disease; glomerulonephritis.
XX
OS   Homo sapiens.
XX
PN   US2004009537-A1.
XX
PD   15-JAN-2004.
XX
PF   13-JAN-2003; 2003US-00342844.
XX
PR   11-JAN-2002; 2002US-0347459P.
PR   02-AUG-2002; 2002US-0401171P.
PR   20-AUG-2002; 2002US-0405678P.
XX
PA   (ROOS/) ROOS J.
PA   (STAU/) STAUDERMAN K.
PA   (VELI/) VELICELEBI G.
XX
PI   Roos J, Stauderman K, Velicelebi G;
XX
DR   WPI; 2004-090465/09.
DR   N-PSDB; ADI81605.
XX
PT   Identifying an agent that modulates intracellular calcium levels, useful
PT   for treating diseases associated with calcium dysregulation (e.g.
PT   cancer), comprises monitoring the effects of the agent on store-operated
PT   calcium entry.
XX
PS   Disclosure; SEQ ID NO 76; 55pp; English.
XX
CC   The invention relates to identifying an agent that modulates
CC   intracellular calcium comprises monitoring the effects of the agent on
CC   store-operated calcium entry comprising contacting one or more test cells
CC   or their portion comprising one or more proteins that is (are) at least
CC   about 35% homologous to the protein encoded by Drosophila gene CG4536 or
CC   CG5842 over at least about 40% of the encoded protein (and that provides
CC   for store-operated calcium entry with a test agent), where the portion of
CC   the cell comprises the proteins, monitoring the effect(s) of the test
CC   compound on store-operated calcium entry and identifying a test agent as
CC   an agent if it has an effect on store-operated calcium entry. Also
CC   included are a method of modulating store-operated calcium entry
CC   (comprising modulating the level of, expression of, activity of or
CC   molecular interactions of a protein in a cell that has altered store-
CC   operated calcium entry, where the protein is at least about 35%
CC   homologous to the protein encoded by Drosophila gene CG4536 or CG5842
CC   over at least about 40% of the encoded protein and that provides for
CC   store-operated calcium transport
CC   into the cell is modulated), and a method of identifying a molecule that
CC   provides for store-operated calcium entry (comprising identifying a
CC   molecule that interacts with the protein mentioned above, thus,
CC   identifying molecules involved in modulating store-operated calcium
CC   entry. The protein does not contain the contiguous sequences appearing as
CC   ADI81644 and ADI81645. The proteins are selected from ion transport
CC   proteins. The method is useful in modulating, or in identifying agents
CC   that modulate, intracellular calcium. These may be used in treating
CC   diseases associated with calcium dysregulation, such as neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
CC   diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
CC   (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
CC   glomerulonephritis). The present sequence represnts an identified
CC   homologue of one of the two above mentioned drosophila proteins.
XX
SQ   Sequence 831 AA;

Query Match             99.2%;  Score 3829;  DB 8;  Length 831;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches   736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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FT                   /label= Transmembrane_domain
FT   Domain          617..635
FT                   /label= Transmembrane_domain
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FT                   /label= Poor_loop_region
FT   Domain          693..720
FT                   /label= Transmembrane_domain
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PN   WO200134805-A2.
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PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US031077.
XX
PR   12-NOV-1999; 99US-00438997.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Masters JN, Vos MH;
XX
DR   WPI; 2001-335930/35.
DR   N-PSDB; AAD05107.
XX
PT   Novel human vanilloid receptor gene and encoded polypeptides for
PT   identifying compounds that modulate vanilloid receptors in human tissues
PT   and for treating inflammation, arthritis, psoriasis and wound healing.
XX
PS   Claim 18; Fig 8; 91pp; English.
XX
CC   The present sequence is human vanilloid receptor 3 (hVR3) protein.
CC   Vanilloid receptor protein and its DNA are useful for identifying
CC   compounds which modulate vanilloid receptors in human tissues, which are
CC   useful for treating various disease states, including neuropathic pain,
CC   inflammation, arthritis, rhinitis, pruritus, bladder dysfunction, cluster
CC   headache, wound healing, and psoriasis. Vanilloid receptor DNA is useful
CC   as standard or reagent in diagnostic immunoassays, as targets for
CC   pharmaceutical screening assays and also in gene therapy. Vanilloid
CC   receptor protein is useful for detecting the presence of anti-vanilloid
CC   receptor derived polypeptide in test samples. Vanilloid receptor
CC   antibodies are useful for detecting vanilloid receptor polypeptides, for
CC   screening for diseases or conditions associated with abnormal vanilloid
CC   receptor production, treating disorders involving capsaicin-sensitive ion
CC   channels and as diagnostic markers
XX
SQ   Sequence 871 AA;

Query Match             99.2%;  Score 3829; DB 4; Length 871;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
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Qy         61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
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Qy        121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
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Db        121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy        181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy        241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
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Db        241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy        301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
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Db        301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy        361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy        421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
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Qy        481 AMVIFFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFNIKDLFMKKCPGV 540
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Qy        541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
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Db        541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy        601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
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Qy        661 RDSETFSTFLDLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILLTFVLLNMLIALMGE 720
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Db        721 TVGQVSKESKHIWKLQ 736
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```
RESULT 3
AAE01227
ID   AAE01227 standard; protein; 871 AA.
XX
AC   AAE01227;
XX
DT   31-JUL-2001 (first entry)
XX
DE   Human vanilloid receptor 3 (hVR3) protein.
XX
KW   Human; vanilloid receptor 3; VR3; inflammation; arthritis; psoriasis;
KW   wound healing; analgesic; vulnerary; antiallergic; gene therapy;
KW   neuropathic pain; rhinitis; pruritus; bladder dysfunction;
KW   cluster headache; capsaicin-sensitive ion channel disorder.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          238..269
FT                   /label= Ankaryn_repeat
```

PT  receptor 3 (VR-3) and VR-5, useful for screening modulators of VR-3 or VR
PT  -5 and for treating calcium homeostasis related disorders (e.g. dementia)
PT  and pain disorders.
XX
PS  Claim 13; Fig 2A-C; 167pp; English.
XX
CC  The invention provides nucleic acid encoding human ion channels referred
CC  to as Vanilloid receptor 3 (VR-3) and VR-5. The VR-3 or VR-5 proteins can
CC  be used to screen for naturally occurring VR-3 or VR-5 ligands or for
CC  drugs or compound which modulate VR-3 or VR-5 activity. The VR-3 or VR-5
CC  proteins and their modulators (e.g. antisense nucleic acids and anti-VR
CC  antibodies) are useful for treating disorders characterized by
CC  insufficient or excessive production of VR-3 or VR-5. These disorders are
CC  calcium homeostasis related disorders (Alzheimer's disease, dementia,
CC  Parkinson's disease) pain disorders (diabetic neuropathy, rheumatoid
CC  arthritis) and/or cellular growth and/or proliferation disorders (e.g.
CC  cancer). Numerous other examples of these disorders are given in the
CC  specification. The present sequence represents the human VR-5
XX
SQ  Sequence 871 AA;

Query Match             99.2%;  Score 3829;  DB 4;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  736;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKRKL 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKRKL 180

Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRPLLVLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRPLLVLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVFFILLVTYIILTFVLLLNMLIALMGE 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVFFILLVTYIILTFVLLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQ 736
         ||||||||||||||||
Db  721 TVGQVSKESKHIWKLQ 736

RESULT 4
AAG65787
ID  AAG65787 standard; protein; 871 AA.
XX
AC  AAG65787;
XX
DT  30-JAN-2002 (first entry)
XX
DE  Human ion channel VR-5 protein sequence.
XX
KW  Ion channel; vanilloid receptor; VR-3; VR-5; nootropic; neuroprotective;
KW  antiparkinsonian; analgesic; antidiabetic; antiproliferative; cytostatic;
KW  antirheumatic; antiarthritic; gene therapy; antisense therapy.
XX
OS  Homo sapiens.
XX
PN  WO200168857-A2.
PD  20-SEP-2001.
XX
PF  15-MAR-2001; 2001WO-US008329.
PR  15-MAR-2000; 2000US-00525420.
XX
PA  (MILL-) MILLENNIUM PHARM INC.
XX
PI  Curtis RAJ, Cook WJ;
XX
DR  WPI; 2001-596911/67.
DR  N-PSDB; AAI66972, AAI66973.
XX
PT  Nucleic acid encoding human ion channels referred to as Vanilloid

```
Qy   721 TVGQVSKESKHIWKLQ 736
         ||||||||||||||||
Db   721 TVGQVSKESKHIWKLQ 736


RESULT 5
AAU74935
ID   AAU74935 standard; protein; 871 AA.
XX
AC   AAU74935;
XX
DT   23-APR-2002  (first entry)
XX
DE   Amino acid sequence of human vanilloid receptor-like protein 2a (VRL-2a).
XX
KW   Human; vanilloid receptor-like protein 2a; VRL-2a; hypertension;
KW   ion-channel protein; pain; osteoarthritis; diabetic neuropathy;
KW   neuralgia; nerve injury; neurodegeneration; stroke; inflammation; asthma;
KW   allergy; urogenital disorder; incontinence; hypotension;
KW   perivascular disease; VRL-related disease; receptor.
XX
OS   Homo sapiens.
XX
PN   EP1160254-A1.
XX
PD   05-DEC-2001.
XX
PF   25-MAY-2001; 2001EP-00304663.
PR   31-MAY-2000; 2000US-0208156P.
XX
PA   (PFIZ ) PFIZER INC.
XX
PI   Shinjo K, Yabuuchi H;
XX
DR   WPI; 2002-084359/12.
DR   N-PSDB; ABK14002.
XX
PT   New human vanilloid receptor-like proteins, useful for identifying
PT   modulators for e.g. treating pain, also related nucleic acid.
XX
PS   Claim 1; Page 17-18; 32pp; English.
XX
CC   The present invention relates to a new polypeptide that has a sequence
CC   871 amino acids (AAU74935) or 602 amino acids (AAU74936) long, or their
CC   variants, as defined in the specification. The polypeptide of the
CC   invention is deduced from a human nucleic acid 2749 base pairs (ABK14002)
CC   or 1900 base pairs (ABK14003) long, or their variants, also defined in
CC   the specification. The polypeptides of the invention, which are human
CC   vanilloid receptor-like (VRL) proteins, are used to identify specific
CC   modulators that are potentially useful for treating pain (of any origin),
CC   osteoarthritis, (diabetic) neuropathy, neuralgia, nerve injury,
CC   neurodegeneration, stroke, inflammation, asthma, allergy, urogenital
CC   disorders, incontinence, hypo- or hyper-tension and perivascular disease.
CC   The molecules of the invention can also be used to raise specific
CC   antibodies. The nucleic acid that encodes the polypeptide of the
CC   invention is useful for recombinant production of the protein and for
CC   preparing transgenic animal models. The polypeptide, antibody and nucleic
CC   acid of the invention are also useful as diagnostic agents for
CC   determining (susceptibility to) VRL-related diseases. The present amino
CC   acid sequence represents the human vanilloid receptor-like protein 2a
CC   (VRL-2a) of the invention
XX
SQ   Sequence 871 AA;

Query Match     99.2%;  Score 3829;  DB 5;  Length 871;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches  736;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
```

```
Qy    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLPFDYGTYRHHSSDN 120
         |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLPFDYGTYRHHSSDN 120

Qy   121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPLFDIVSRGSTADLDGLLPFLLTHKKRL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPLFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy   301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy   421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy   481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLLFTGVLFFFTNIKDLFMKKCPGV 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLLFTGVLFFFTNIKDLFMKKCPGV 540

Qy   541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy   601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASAALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASAALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy   661 RDSETFSTFLLDLFKLITGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 RDSETFSTFLLDLFKLITGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720

Qy   721 TVGQVSKESKHIWKLQ 736
         ||||||||||||||||
Db   721 TVGQVSKESKHIWKLQ 736


RESULT 6
ABB79191
ID   ABB79191 standard; protein; 871 AA.
XX
AC   ABB79191;
XX
DT   07-AUG-2002  (first entry)
XX
DE   Human VR4 protein SEQ ID NO:2.
XX
KW   Human; VR4; vanilloid 4 receptor; receptor; osteopathic; antirheumatic;
KW   antiarthritic; vulnerary; analgesic; gene therapy; cartilage; bone;
KW   larynx; auditory canal; intravertebral disc; ligament; tendon;
KW   joint capsule; bone development disorder; osteoporosis; osteoarthritis;
KW   joint destruction; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   WO200234280-A2.
XX
PD   02-MAY-2002.
XX
PF   25-OCT-2001; 2001WO-GB004739.
XX
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Qy  601 TYSIMIQKILFKDLFRFLLVYILFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYILFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQ 736
        ||||||||||||||||
Db  721 TVGQVSKESKHIWKLQ 736
```

RESULT 7
ADG64947
ID   ADG64947 standard; protein; 871 AA.
XX
AC   ADG64947;
XX
DT   11-MAR-2004  (first entry)
XX
DE   VANILREP4 polypeptide of the invention.
XX
KW   vanilrep4; VR4; Analgesic; cerebroprotective; antiinflammatory;
KW   antidiabetic; anorectic; vasotropic; uropathic; ischemia;
KW   neurodegeneration; inflammatory disorder; irritable bowel syndrome;
KW   diabetes; obesity.
XX
OS   Homo sapiens.
XX
PN   EP1170365-A1.
XX
PD   09-JAN-2002.
XX
PF   04-JUL-2000; 2000EP-00202352.
XX
PR   04-JUL-2000; 2000EP-00202352.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Smith G, Hayes PD, Smart D, Davis JB, Kelsell RE;
XX
DR   WPI; 2002-156636/21.
DR   N-PSDB; ADG64946.
XX
PT   Polypeptide of ion channel family polypeptides, designated vanilrep4,
PT   useful as a vaccine for inducing immune response against diseases such as
PT   neuropathies, algesia, nerve injury, ischemia, stroke, incontinence,
PT   diabetes, obesity.
XX
PS   Claim 1; SEQ ID NO 2; 29pp; English.
XX
CC   The present invention relates to a polypeptide of ion channel family
CC   polypeptides, vanilrep4 (VR4). The peptides are useful for treating pain
CC   (e.g. chronic pain, neuropathic pain, post-operative pain, rheumatoid
CC   arthritic pain), neuralgia, neuropathies, algesia, nerve injury,
CC   ischemia, neurodegeneration, stroke, incontinence, inflammatory
CC   disorders, irritable bowel syndrome, diabetes or obesity. Fragments of
CC   the protein are useful for producing full-length polypeptides by peptide
CC   synthesis therefore the variants may also be employed as intermediate for
CC   producing full-length polypeptide. The proteins are also useful for
CC   identifying agonists or antagonists of peptide activity and expression.
CC   The peptide is useful as diagnostic reagents for diagnosing a disease or
CC   a susceptibility to a disease by detecting mutations in the associated
CC   gene, and is also useful for chromosome localization studies and tissue
CC   expression studies. The peptide is useful for producing transgenic
CC   animals, which include knock-in animals (in which an animal gene is
CC   replaced by human equivalent within the genome of the animal), useful in
CC   drug discovery process, for target validation, where the compound is
CC   specific for human target. Peptides and Ab is useful for configuring
CC   screening methods for detecting the effect of added compounds on the
CC   production of mRNA in cells. The peptides are useful as vaccines for

PR   25-OCT-2000; 2000GB-00026114.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Davis JB, Gunthorpe MJ, Egerton J, Smart D;
XX
DR   WPI; 2002-471426/50.
DR   N-PSDB; ABN87645.
XX
PT   Use of vanilloid 4 receptor polypeptide/polynucleotide, a modulator of
PT   the polypeptide or an antisense polynucleotide to the polynucleotide, for
PT   manufacture of a medicament for treating cartilage and/or bone diseases.
XX
PS   Claim 8; Page 22; 30pp; English.
XX
CC   The present sequence represents human vanilloid 4 receptor (VR4). VR4 has
CC   osteopathic, antirheumatic, antiarthritic, vulnerary and analgesic
CC   activities. VR4 proteins and polynucleotide sequences can be used in
CC   modulating VR4 activity, in gene therapy and in antisense gene therapy.
CC   VR4 is useful for the manufacture of a medicament for treating diseases
CC   of cartilage and/or bone, or for the treatment of pain associated with
CC   it, where the disease is one affecting the larynx, auditory canal,
CC   intravertebral discs, ligaments, tendons and joint capsules, or a disease
CC   associated with bone development including osteoporosis, or diseases
CC   involving joint destruction such as rheumatoid arthritis or
CC   osteoarthritis, and the pain is associated with rheumatoid arthritis or
CC   osteoarthritis.
XX
SQ   Sequence 871 AA;

```
Query Match             99.2%;  Score 3829;  DB 5;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches   736;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEARPLSSLANLFEGEDGSLSPSPADASRPAGP 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEARPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFTNIKDLFMKKCCPGV 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFTNIKDLFMKKCCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
```

KW   TRPV7; TRPV4; VRL3; OTRPC4; TRPM8; TRPX; trkA+; inflammation;
KW   skin disorder; cancer; analgesic; antiinflammatory; dermatological;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2002101045-A2.
XX
PD   19-DEC-2002.
XX
PF   13-JUN-2002; 2002WO-EP006520.
XX
PR   13-JUN-2001; 2001US-0297835P.
PR   22-JAN-2002; 2002US-0351238P.
PR   29-JAN-2002; 2002US-0352914P.
PR   12-FEB-2002; 2002US-0357161P.
PR   15-MAY-2002; 2002US-0381086P.
PR   16-MAY-2002; 2002US-0381739P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (IRMI-) IRM LLC.
XX
PI   Patapoutian A, Song C, Ganju P, Peier A, Mcintyre P, Bevan S;
XX
DR   WPI; 2003-156962/15.
DR   N-PSDB; ADG32561.
XX
PT   New isolated TRPV3, TRPV4 or TRPM8 vanilloid receptor nucleic acid
PT   molecule and polypeptides, useful for the diagnosis and treatment of
PT   disorders such as pain, inflammation, skin diseases and cancer.
XX
PS   Claim 69; SEQ ID NO 17; 197pp; English.
XX
CC   This invention relates to novel vanilloid receptor (VR) related nucleic
CC   acids and encoded proteins thereof. Specifically, it refers to certain
CC   members of the VR family that are involved in pain perception, in
CC   particular, TRPV3 (previously known as VRLS, VRLX, VR4 & TRPV7), TRPV4
CC   (previously known as VRL3 & OTRPC4) and TRPM8 (previously known as TRPX).
CC   Furthermore, this invention includes trkA+ pain specific genes expressed
CC   in the sensory neurons of the dorsal root ganglia. Accordingly, such
CC   compositions can be useful for the diagnosis, treatment and prevention of
CC   pain, inflammation, skin disorders and cancer, and so exhibit analgesic,
CC   antiinflammatory, dermatological and cytostatic activities. This
CC   polypeptide sequence is the human TRPV4 protein of the invention.
XX
SQ   Sequence 871 AA;

Query Match             99.2%;  Score 3829;  DB 7;  Length 871;
Best Local Similarity   100.0%;
Matches  736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```
Qy    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60

Qy   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120

Qy  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPLFDIVSRGSTADLDGLLPFLLTHKKRL  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPLFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300

Qy  301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
```

CC   inducing an immunological response in a mammal. The present sequence
CC   represents VANILREP4 polypeptide.
XX
SQ   Sequence 871 AA;

Query Match             99.2%;  Score 3829;  DB 5;  Length 871;
Best Local Similarity   100.0%;
Matches  736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```
Qy    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60

Qy   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120

Qy  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPLFDIVSRGSTADLDGLLPFLLTHKKRL  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPLFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300

Qy  301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360

Qy  361  NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420

Qy  421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480

Qy  481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFNIKDLFMKKCPGV  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFNIKDLFMKKCPGV  540

Qy  541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600

Qy  601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660

Qy  661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILLTFVLLNMLIALMGE  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILLTFVLLNMLIALMGE  720

Qy  721  TVGQVSKESKHIWKLQ  736
         ||||||||||||||||
Db  721  TVGQVSKESKHIWKLQ  736
```

RESULT 8
ADG32562
ID   ADG32562  standard; protein; 871 AA.
XX
AC   ADG32562;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human TRPV4 protein, member of the vanilloid receptor family.
XX
KW   human; vanilloid receptor; VR; pain perception; TRPV3; VRLS; VRLX; VR4;

```
CC    ingredient. The proteins, genes, agents and methods are useful for
CC    preventing and treating a cartilage disease, e.g. osteoarthritis,
CC    cartilage defect, or rheumatoid arthritis. The current sequence
CC    represents a human protein that promotes type II collagen expression.
XX
SQ    Sequence 871 AA;

Query Match             99.2%;  Score 3829;  DB 7;  Length 871;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches  736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy         61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy        121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy        181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy        241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300

Qy        301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy        361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy        421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy        481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy        541 NSLFIDGSFQLLYFIYSVLIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 NSLFIDGSFQLLYFIYSVLIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy        601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy        661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720

Qy        721 TVGQVSKESKHIWKLQ 736
              ||||||||||||||||
Db        721 TVGQVSKESKHIWKLQ 736


RESULT 9
ADL71047
ID   ADL71047 standard; protein; 871 AA.
XX
AC   ADL71047;
XX
DT   20-MAY-2004 (first entry)
XX
DE   Type II collagen expression promoting protein, seq id 40.
XX
KW   Osteopathic; antiinflammatory; antirheumatic; antiarthritic;
KW   gene therapy; type II collagen; expression; cartilage disease;
KW   osteoarthritis; cartilage defect; rheumatoid arthritis; human.
XX
OS   Homo sapiens.
XX
PN   WO200308375-A1.
XX
PD   23-OCT-2003.
XX
PF   16-APR-2003; 2003WO-JP004802.
PR   16-APR-2002; 2002JP-00113908.
PR   19-APR-2002; 2002US-0373594P.
XX
PA   (ASAH ) ASAHI KASEI KK.
XX
PI   Matsuda A, Honda G, Muramatsu S;
XX
DR   WPI; 2003-845331/78.
DR   N-PSDB; ADL71046.
XX
PT   New purified protein that promotes type II collagen expression, useful
PT   for preventing and treating a cartilage disease, e.g. osteoarthritis,
PT   cartilage defect, or rheumatoid arthritis.
XX
PS   Claim 1; SEQ ID NO 40; 271pp; English.
XX
CC   The invention relates to a purified protein (I) that promotes type II
CC   collagen expression. Also disclosed is an isolated polynucleotide
CC   encoding (I), a recombinant vector comprising the polynucleotide and a
CC   gene therapeutic agent comprising the recombinant vector as an active


RESULT 10
ADI81584
ID   ADI81584 standard; protein; 871 AA.
XX
AC   ADI81584;
XX
DT   22-APR-2004 (first entry)
XX
DE   Human vanilloid receptor-related channel like protein.
```

```
XX
KW   Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
KW   neurological disease; inflammatory disease; cancer; Alzheimer's disease;
KW   Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
KW   hepatitis; cirrhosis; kidney disease; glomerulonephritis.
XX
OS   Homo sapiens.
XX
PN   US2004009537-A1.
XX
PD   15-JAN-2004.
XX
PF   13-JAN-2003; 2003US-00342844.
XX
PR   11-JAN-2002; 2002US-0347459P.
PR   02-AUG-2002; 2002US-0401171P.
PR   20-AUG-2002; 2002US-0405678P.
XX
PA   (ROOS/) ROOS J.
PA   (STAU/) STAUDERMAN K.
PA   (VELI/) VELICELEBI G.
XX
PI   Roos J,  Stauderman K,  Velicelebi G;
XX
DR   WPI; 2004-090465/09.
DR   N-PSDB; ADI81583.
XX
PT   Identifying an agent that modulates intracellular calcium levels, useful
PT   for treating diseases associated with calcium dysregulation (e.g.
PT   cancer), comprises monitoring the effects of the agent on store-operated
PT   calcium entry.
XX
PS   Disclosure; SEQ ID NO 54; 55pp; English.
XX
CC   The invention relates to identifying an agent that modulates
CC   intracellular calcium comprises monitoring the effects of the agent on
CC   store-operated calcium entry comprising contacting one or more test cells
CC   or their portion comprising one or more proteins that is (are) at least
CC   about 35% homologous to the protein encoded by Drosophila gene CG4536 or
CC   CG5842 over at least about 40% of the encoded protein (and that provides
CC   for store-operated calcium entry with a test agent), where the portion of
CC   the cell comprises the proteins, monitoring the effect(s) of the test
CC   compound on store-operated calcium entry and identifying a test agent as
CC   an agent if it has an effect on store-operated calcium entry. Also
CC   included are a method of modulating store-operated calcium entry
CC   (comprising modulating the level of, expression of, activity of or
CC   molecular interactions of a protein in a cell that has altered store-
CC   operated calcium entry, where the protein is at least about 35%
CC   homologous to the protein encoded by Drosophila gene CG4536 or CG5842
CC   over at least about 40% of the encoded protein and that provides for
CC   store-operated calcium entry, and where store-operated calcium transport
CC   into the cell is modulated) and a method of identifying a molecule that
CC   provides for store-operated calcium entry (comprising identifying a
CC   molecule that interacts with the protein mentioned above, thus,
CC   identifying molecules involved in modulating store-operated calcium
CC   entry. The protein does not contain the contiguous sequences appearing as
CC   ADI81644 and ADI81645. The proteins are selected from ion transport
CC   proteins. The method is useful in modulating, or in identifying agents
CC   that modulate, intracellular calcium. These may be used in treating
CC   diseases associated with calcium dysregulation, such as neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
CC   diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
CC   (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
CC   glomerulonephritis). The present sequence represents an identified
CC   homologue of one of the two above mentioned drosophila proteins.
XX
SQ   Sequence 871 AA;

Query Match             99.2%;  Score 3829;  DB 8;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
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Db           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy         61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy        121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy        181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy        241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFGELPLSLAACTNQPHI 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFGELPLSLAACTNQPHI 300

Qy        301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy        361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy        421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy        481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy        541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy        601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy        661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720

Qy        721 TVGQVSKESKHIWKLQ 736
             ||||||||||||||||
Db        721 TVGQVSKESKHIWKLQ 736
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RESULT 11
ADI81608
ID   ADI81608 standard; protein; 871 AA.
XX
AC   ADI81608;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human OTRPC4 cation channel.
XX
KW   Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
KW   neurological disease; inflammatory disease; cancer; Alzheimer's disease;
KW   Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
KW   hepatitis; cirrhosis; kidney disease; glomerulonephritis.
XX
OS   Homo sapiens.
XX
PN   US2004009537-A1.
XX
PD   15-JAN-2004.
XX
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Db  181 TDEBFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQOHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQOHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
Qy  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
Qy  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASAALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASAALVSLLNPCANMKVCNEDQTNCTVPTYPSC 669
Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
Qy  721 TVGQVSKESKHIWKLQ 736
            ||||||||||||||||
Db  721 TVGQVSKESKHIWKLQ 736
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RESULT 12
ADI81588
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ID   ADI81588 standard; protein; 871 AA.
XX
AC   ADI81588;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human vanilloid receptor-like channel 2.
XX
KW   Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
KW   neurological disease; inflammatory disease; cancer; Alzheimer's disease;
KW   Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
KW   hepatitis; cirrhosis; kidney disease; glomerulonephritis.
XX
OS   Homo sapiens.
XX
PN   US2004009537-A1.
XX
PD   15-JAN-2004.
XX
PF   13-JAN-2003; 2003US-00342844.
XX
PR   11-JAN-2002; 2002US-0347459P.
PR   02-AUG-2002; 2002US-0401171P.
PR   20-AUG-2002; 2002US-0405678P.
XX
PA   (ROOS/) ROOS J.
PA   (STAU/) STAUDERMAN K.
PA   (VELI/) VELICELEBI G.
XX
PI   Roos J, Stauderman K, Velicelebi G;
XX
DR   WPI; 2004-090465/09.
DR   N-PSDB; ADI81607.
XX
PT   Identifying an agent that modulates intracellular calcium levels, useful
PT   for treating diseases associated with calcium dysregulation (e.g.
PT   cancer), comprises monitoring the effects of the agent on store-operated
PT   calcium entry.
XX
PS   Disclosure; SEQ ID NO 78; 55pp; English.
XX
CC   The invention relates to identifying an agent that modulates
CC   intracellular calcium comprises monitoring the effects of the agent on
CC   store-operated calcium entry comprising contacting one or more test cells
CC   or their portion comprising one or more proteins that is (are) at least
CC   about 35% homologous to the protein encoded by Drosophila gene CG4536 or
CC   CG5842 over at least about 40% of the encoded protein (and that provides
CC   for store-operated calcium entry with a test agent), where the portion of
CC   the cell comprises the proteins, monitoring the effect(s) of the test
CC   compound on store-operated calcium entry and identifying a test agent as
CC   an agent if it has an effect on store-operated calcium entry. Also
CC   included are a method of modulating store-operated calcium entry
CC   (comprising modulating the level of, expression of, activity of or
CC   molecular interactions of a protein in a cell that has altered store-
CC   operated calcium entry, where the protein is at least about 35%
CC   homologous to the protein encoded by Drosophila gene CG4536 or CG5842
CC   over at least about 40% of the encoded protein and that provides for
CC   store-operated calcium transport into the cell is modulated) and a method of identifying a molecule that
CC   provides for store-operated calcium entry (comprising identifying a
CC   molecule that interacts with the protein mentioned above, thus
CC   identifying molecules involved in modulating store-operated calcium
CC   entry. The protein does not contain the contiguous sequences appearing as
CC   ADI81644 and ADI81645. The proteins are selected from ion transport
CC   proteins. The method is useful in modulating, or in identifying agents
CC   that modulate, intracellular calcium. These may be used in treating
CC   diseases associated with calcium dysregulation, such as neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
CC   diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
CC   (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
CC   glomerulonephritis). The present sequence represents an identified
CC   homologue of one of the two above mentioned drosophila proteins.
XX
SQ   Sequence 871 AA;
```

```
Query Match             99.2%;  Score 3829;  DB 8;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  736;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
Qy  121 KRWRKKIIEKOPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADDLGLLPFLLTHKKRL 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKOPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADDLGLLPFLLTHKKRL 180
Qy  181 TDEBFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
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DR   WPI; 2004-090465/09.
DR   N-PSDB; ADI81587.
XX
PT   Identifying an agent that modulates intracellular calcium levels, useful
PT   for treating diseases associated with calcium dysregulation (e.g.
PT   cancer), comprises monitoring the effects of the agent on store-operated
PT   calcium entry.
XX
PS   Disclosure; SEQ ID NO 58; 55pp; English.
XX
CC   The invention relates to identifying an agent that modulates
CC   intracellular calcium comprises monitoring the effects of the agent on
CC   store-operated calcium entry comprising contacting one or more test cells
CC   or their portion comprising one or more proteins that is (are) at least
CC   about 35% homologous to the protein encoded by Drosophila gene CG4536 or
CC   CG5842 over at least about 40% of the encoded protein (and that provides
CC   for store-operated calcium entry with a test agent), where the portion of
CC   the cell comprises the proteins, monitoring the effect(s) of the test
CC   compound on store-operated calcium entry and identifying a test agent as
CC   an agent if it has an effect on store-operated calcium entry. Also
CC   included are a method of modulating store-operated calcium entry
CC   (comprising modulating the level of, expression of, activity of or
CC   molecular interactions of a protein in a cell that has altered store-
CC   operated calcium entry, where the protein is at least about 35%
CC   homologous to the protein encoded by Drosophila gene CG4536 or CG5842
CC   over at least about 40% of the encoded protein and that provides for
CC   store-operated calcium entry, and where store-operated calcium transport
CC   into the cell is modulated) and a method of identifying a molecule that
CC   provides for store-operated calcium entry (comprising identifying a
CC   molecule that interacts with the protein mentioned above, thus,
CC   identifying molecules involved in modulating store-operated calcium
CC   entry. The protein does not contain the contiguous sequences appearing as
CC   ADI81644 and ADI81645. The proteins are selected from ion transport
CC   proteins. The method is useful in modulating, or in identifying agents
CC   that modulate, intracellular calcium. These may be used in treating
CC   diseases associated with calcium dysregulation, such as neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
CC   diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
CC   (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
CC   glomerulonephritis). The present sequence represents an identified
CC   homologue of one of the two above mentioned drosophila proteins.
XX
SQ   Sequence 871 AA;

Query Match             99.2%;  Score 3829;  DB 8;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  736;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60

Qy     61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGKKAPMDSLFDYGTYRHHSSDN  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGKKAPMDSLFDYGTYRHHSSDN  120

Qy    121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy    181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy    241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300

Qy    301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360

Qy    361  NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420

Qy    421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480

Qy    481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLLFTGVLFFTNIKDLFMKKCPGV  540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLLFTGVLFFFTNIKDLFMKKCPGV  540

Qy    541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600

Qy    601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASAIVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASAIVSLLNPCANMKVCNEDQTNCTVPTYPSC  660

Qy    661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE  720

Qy    721  TVGQVSKESKHIWKLQ  736
           ||||||||||||||||
Db    721  TVGQVSKESKHIWKLQ  736

RESULT 13
ABB98197
ID   ABB98197 standard; protein; 871 AA.
XX
AC   ABB98197;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human VR-OAC amino acid sequence.
XX
KW   Human; VR-OAC; vanilloid receptor-related osmotically activated channel;
KW   anti-HIV; antiasthmatic; immunomodulator; cerebroprotective;
KW   antidiabetic; antiinfertility; auditory; antipruritic; dermatological;
KW   antipsoriatic; antiallergic; anorectic; neuroprotective;
KW   ophthalmological; nootropic; cytostatic; nephrotropic; hypotensive;
KW   analgesic; mechanoreception; mechanosensation; hearing disorder; HIV;
KW   Human Immunodeficiency virus; obesity; vertigo; motion sickness;
KW   neurological disorder; ataxia; male infertility; immune dysfunction;
KW   diabetes mellitus; chronic obstructive lung disorder; bronchial asthma;
KW   sexual dysfunction; blindness; skin disorder; psoriasis; kidney disease;
KW   arterial hypertension; pain syndrome; Alzheimer's disease; dementia;
KW   hydrocephalus; alopecia; baldness; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200259152-A2.
XX
PD   01-AUG-2002.
XX
PF   26-OCT-2001; 2001WO-US050539.
XX
PR   26-OCT-2000; 2000US-0243568P.
PR   25-OCT-2001; 2001US-00243568.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Liedtke W, Heller S, Hudspeth AJ,  Friedman JM;
XX
DR   WPI; 2002-599762/64.
DR   N-PSDB; ABQ79489.
XX
PT   Modulating mechanoreception or mechanosensation, for diagnosing,
PT   preventing or treating e.g. hearing disorders, HIV or obesity, comprises
PT   administering a vanilloid receptor-related osmotically activated channel
PT   polypeptide.

```
XX
PS   Claim 2; Fig 2; 154pp; English.
XX
CC   The invention relates to modulating mechanoreception/mechanosensation in
CC   a mammal by administering a vanilloid receptor-related osmotically
CC   activated channel (VR-OAC) polypeptide, its active fragments or portions,
CC   or by introducing a nucleic acid vector capable of expressing the VR-OAC
CC   polypeptide. The method of the invention is useful for modulating
CC   mechanoreception or mechanosensation, for diagnosing, preventing or
CC   treating e.g. hearing disorders, Human Immunodeficiency virus (HIV),
CC   obesity, vertigo of labyrinthine origin including motion sickness,
CC   neurological disorders including ataxia, male infertility, immune
CC   dysfunction, diabetes mellitus, chronic obstructive lung disorder,
CC   bronchial asthma, sexual dysfunction, blindness due to corneal or retinal
CC   causes, or skin disorders including psoriasis. Other conditions include
CC   arterial hypertension, kidney diseases, pain syndromes, Alzheimer's
CC   disease and other dementias, hydrocephalus, alopecia, baldness and
CC   cancer. The VR-OAC may be used in detecting or assessing osmotic and
CC   mechanical stimuli, or as the facilitating component in translating an
CC   osmotic or mechanical stimulus in nano-technological, biosensor or
CC   biorobotic devices. The current sequence represents the amino acid
CC   sequence of human VR-OAC as determined from HEK293 cells. NOTE: The
CC   inventors indicate the presence of further VR-OAC polypeptides other than
CC   those given in records AB98197-8. However, no sequence information
CC   regarding these polypeptides which are referred to as SEQ ID's 5, 6, 7, 8
CC   and 9 is given
XX
SQ   Sequence 871 AA;

Query Match             99.2%;  Score 3828;  DB 5;  Length 871;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches  735;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60

Qy     61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy    121 KRWRKKIIEKQPQSPKAPAPOPPPILKVFNRRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy    181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPPRDIYYRGQT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy    241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy    301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy    361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
          ||||||||||||||||||||||||:|:||||||||||||||||||||||||||||||||
Db    361 NLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy    421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy    481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy    541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
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```
Qy    601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy    661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720

Qy    721 TVGQVSKESKHIWKLQ 736
          ||||||||||||||||
Db    721 TVGQVSKESKHIWKLQ 736
```

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RESULT 14
ADI81590
ID   ADI81590 standard; protein; 871 AA.
XX
AC   ADI81590;
XX
DT   22-APR-2004  (first entry)
DE   Human vanilloid receptor-related channel protein #1.
XX
KW   Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
KW   neurological disease; inflammatory disease; cancer; Alzheimer's disease;
KW   Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
KW   hepatitis; cirrhosis; kidney disease; glomerulonephritis.
XX
OS   Homo sapiens.
XX
PN   US2004009537-A1.
XX
PD   15-JAN-2004.
XX
PF   13-JAN-2003; 2003US-0342844.
XX
PR   11-JAN-2002; 2002US-0347459P.
PR   02-AUG-2002; 2002US-0401171P.
PR   20-AUG-2002; 2002US-0405678P.
XX
PA   (ROOS/) ROOS J.
PA   (STAU/) STAUDERMAN K.
PA   (VELI/) VELICELEBI G.
XX
PI   Roos J,  Stauderman K,  Velicelebi G;
XX
DR   WPI; 2004-090465/09.
DR   N-PSDB; ADI81589.
XX
PT   Identifying an agent that modulates intracellular calcium levels, useful
PT   for treating diseases associated with calcium dysregulation (e.g.
PT   cancer), comprises monitoring the effects of the agent on store-operated
PT   calcium entry.
XX
PS   Disclosure; SEQ ID NO 60; 55pp; English.
XX
CC   The invention relates to identifying an agent that modulates
CC   intracellular calcium comprises monitoring the effects of the agent on
CC   store-operated calcium entry comprising contacting one or more test cells
CC   or their portion comprising one or more proteins that is (are) at least
CC   about 35% homologous to the protein encoded by Drosophila gene CG4536 or
CC   CG5842 over at least about 40% of the encoded protein (and that provides
CC   for store-operated calcium entry with a test agent), where the portion of
CC   the cell comprises the proteins, monitoring the effect(s) of the test
CC   compound on store-operated calcium entry and identifying a test agent as
CC   an agent if it has an effect on store-operated calcium entry Also
CC   included are a method of modulating store-operated calcium entry
CC   (comprising modulating the level of, expression of, activity of or
CC   molecular interactions of a protein in a cell that has altered store-
CC   operated calcium entry, where the protein is at least about 35%
CC   homologous to the protein encoded by Drosophila gene CG4536 or CG5842
CC   over at least about 40% of the encoded protein and that provides for
CC   store-operated calcium entry, and where store-operated calcium transport
```

```
CC    into the cell is modulated) and a method of identifying a molecule that
CC    provides for store-operated calcium entry (comprising identifying a
CC    molecule that interacts with the protein mentioned above, thus,
CC    identifying molecules involved in modulating store-operated calcium
CC    entry. The protein does not contain the contiguous sequences appearing as
CC    ADI81644 and ADI81645. The proteins are selected from ion transport
CC    proteins. The method is useful in modulating, or in identifying agents
CC    that modulate, intracellular calcium. These may be used in treating
CC    diseases associated with calcium dysregulation, such as neurodegenerative
CC    diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
CC    diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
CC    (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
CC    glomerulonephritis). The present sequence represnts an identified
CC    homologue of one of the two above mentioned drosophila proteins.
XX
SQ    Sequence 871 AA;

Query Match             99.2%;  Score 3828;  DB 8;  Length 871;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches  735;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy       1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy      61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy     121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy     181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy     241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300

Qy     301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy     361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
           |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db     361 NLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy     421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy     481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy     541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy     601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     661 RDSETFSTFLLDLFKLITGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
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Qy     721 TVGQVSKESKHIWKLQ 736
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RESULT 15
ADE08372
ID   ADE08372 standard; protein; 970 AA.
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AC   ADE08372;
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DT   29-JAN-2004  (first entry)
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DE   Novel protein (useful for identifying genetic disorders) #527.
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KW   novel gene; novel protein; tissue marker; molecular weight marker;
KW   chromosome marker; genetic disorder.
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OS   Unidentified.
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PN   WO2003054152-A2.
XX
PD   03-JUL-2003.
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PF   10-DEC-2002; 2002WO-US039555.
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PR   10-DEC-2001; 2001US-0339739P.
PR   11-DEC-2001; 2001US-0339453P.
PR   14-MAR-2002; 2002US-0365091P.
PR   14-MAR-2002; 2002US-0365384P.
PR   12-APR-2002; 2002US-0372381P.
PR   12-APR-2002; 2002US-0372615P.
PR   22-APR-2002; 2002US-00128558.
PR   24-APR-2002; 2002US-0376045P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,   Asundi V,  Goodrich RW,  Ren F,  Zhang J,  Zhao QA,  Wang J;
PI   Ghosh M,   Xue AJ,  Wehrman T,  Weng G,  Zhou P,  Drmanac RT,  Wang Z;
PI   Ma Y,   Wang D,  Chen R,  Xu C,  Boyle BJ;
XX
DR   WPI; 2003-569235/53.
DR   N-PSDB; ADE07461.
XX
PT   New polynucleotides, useful for expressing recombinant proteins for
PT   analysis, characterization or therapeutic use, or as markers for tissues
PT   in which the corresponding protein is preferentially expressed.
XX
PS   Claim 20; SEQ ID NO 1438; 1177pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of novel
CC   proteins. The DNA and protein sequences of the invention are useful as:
CC   markers for tissues in which the corresponding protein is preferentially
CC   expressed; as molecular weight markers on gels; as chromosome markers or
CC   tags; to identify chromosomes or to map related gene positions; and to
CC   compare with endogenous DNA sequences in patients to identify potential
CC   genetic disorders. The present amino acid sequence represents a protein
CC   of the invention.
XX
SQ   Sequence 970 AA;

Query Match             99.2%;  Score 3828;  DB 7;  Length 970;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches  735;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy     121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
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Db   340  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  399

Qy   301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
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Db   400  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  459

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Qy   541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
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Db   640  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  699

Qy   601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
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Qy   661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE  720
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Qy   721  TVGQVSKESKHIWKLQ  736
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Db   820  TVGQVSKESKHIWKLQ  835
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Search completed: May  4, 2005, 22:15:21
Job time : 177 secs

# Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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OM protein - protein search, using sw model

Copyright  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:      May  4, 2005, 22:10:59 ; Search time 43 Seconds
                                      (without alignments)
                                      1288.130 Million cell updates/sec

Title:         US-10-090-215-12
Perfect score: 3858
Sequence:    1 MADSSEGPRAGPGEVAELPG.........GQVSKESKHIWKLQSGRRRL 742

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    513545 seqs, 7649064 residues

Total number of hits satisfying chosen parameters:      513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Issued Patents AA:*
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               2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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               4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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               6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match Score | Query Match Length | DB | ID | Description |
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| 1 | 3858 | 100.0 | 742 | 4 | US-09-500-123-12 | Sequence 12, Appli |
| 2 | 3823 | 99.1 | 871 | 4 | US-09-500-123-7 | Sequence 7, Appli |
| 3 | 3470 | 89.9 | 811 | 4 | US-09-500-123-9 | Sequence 9, Appli |
| 4 | 1604.5 | 41.6 | 843 | 3 | US-09-235-451-25 | Sequence 25, Appl |
| 5 | 1604.5 | 41.6 | 843 | 4 | US-09-978-303-25 | Sequence 25, Appl |
| 6 | 1579.5 | 40.9 | 838 | 3 | US-09-235-451-2 | Sequence 2, Appl |
| 7 | 1579.5 | 40.9 | 838 | 4 | US-09-132-316-3 | Sequence 3, Appli |
| 8 | 1579.5 | 40.9 | 838 | 4 | US-09-667-422-9 | Sequence 9, Appli |
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| 10 | 1557.5 | 40.4 | 839 | 3 | US-09-197-636-2 | Sequence 2, Appli |
| 11 | 1556.5 | 40.3 | 839 | 4 | US-09-197-636-8 | Sequence 8, Appli |
| 12 | 1556.5 | 40.3 | 839 | 3 | US-09-235-451-34 | Sequence 34, Appl |
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| 19 | 1324 | 34.3 | 761 | 3 | US-09-235-451-4 | Sequence 4, Appli |
| 20 | 1324 | 34.3 | 761 | 4 | US-09-978-303-4 | Sequence 4, Appli |
| 21 | 1306 | 33.9 | 889 | 4 | US-09-132-316-2 | Sequence 2, Appl |
| 22 | 1298.5 | 33.7 | 764 | 3 | US-09-235-451-36 | Sequence 36, Appl |
| 23 | 1298.5 | 33.7 | 764 | 4 | US-09-978-303-36 | Sequence 36, Appl |
| 24 | 1071 | 27.8 | 511 | 4 | US-09-667-422-5 | Sequence 5, Appli |
| 25 | 777 | 20.1 | 727 | 3 | US-09-235-451-23 | Sequence 23, Appl |
| 26 | 777 | 20.1 | 727 | 4 | US-09-978-303-23 | Sequence 23, Appl |
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| 28 | 724.5 | 18.8 | 725 | 4 | US-09-350-457A-2 | Sequence 2, Appli |
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| 30 | 521 | 13.5 | 511 | 4 | US-09-759-143-909 | Sequence 909, App |
| 31 | 227 | 5.9 | 71 | 3 | US-09-235-451-14 | Sequence 14, Appl |
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| 33 | 221.5 | 5.7 | 1709 | 4 | US-09-392-812A-6 | Sequence 6, Appli |
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| 35 | 215 | 5.6 | 1165 | 4 | US-09-949-016-11392 | Sequence 11392, A |
| 36 | 213 | 5.5 | 134 | 4 | US-09-759-143-910 | Sequence 910, App |
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| 38 | 180 | 4.7 | 1704 | 2 | US-09-392-812A-2 | Sequence 2, Appli |
| 39 | 172 | 4.5 | 1095 | 3 | US-09-112-096-15 | Sequence 15, Appl |
| 40 | 172 | 4.5 | 1095 | 4 | US-09-636-215-778 | Sequence 778, App |
| 41 | 172 | 4.5 | 1095 | 4 | US-09-685-166A-778 | Sequence 778, App |
| 42 | 172 | 4.5 | 1095 | 4 | US-09-679-426-778 | Sequence 778, App |
| 43 | 172 | 4.5 | 1095 | 4 | US-09-759-143-778 | Sequence 778, App |
| 44 | 172 | 4.5 | 1095 | 4 | US-09-651-236-778 | Sequence 778, App |
| 45 | 169 | 4.4 | 1095 | 4 | US-09-636-215-780 | Sequence 780, App |

ALIGNMENTS

RESULT 1
US-09-500-123-12
; Sequence 12, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
;   APPLICANT: Dubin, Adrienne E
;   APPLICANT: Huvar, Arne
;   APPLICANT: Erlander, Mark G
;   APPLICANT: Glass, Charles A
;   TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor
;   TITLE OF INVENTION: VR3
;   FILE REFERENCE: Human VR3 receptors
;   CURRENT APPLICATION NUMBER: US/09/500,123
;   CURRENT FILING DATE: 2000-02-08
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 742
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-500-123-12

Query Match             100.0%;  Score 3858;  DB 4;  Length 742;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  742;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
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Qy    181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
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Qy   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
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Qy   601 TYSIMIQKILFKDLFRFLLVYLLFMIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 660
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Qy   661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIIILLVTYIILTFVLLNMLIALMGE 720
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Db   661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIIILLVTYIILTFVLLNMLIALMGE 720

Qy   721 TVGQVSKESKHIWKLQ 736
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Db   721 TVGQVSKESKHIWKLQ 736
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RESULT 3
US-09-500-123-9

; Sequence 9, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 9
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-9

Query Match          89.9%;  Score 3470;  DB 4;  Length 811;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 675; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
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RESULT 2
US-09-500-123-7

; Sequence 7, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-7

Query Match          99.1%;  Score 3823;  DB 4;  Length 871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 735; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

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Db    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy   121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
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Db   121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Qy   181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPPRDIYYRGQT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPPRDIYYRGQT  240

Qy   241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI   300

Qy   301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360

Qy   361  NLEAVLNNDGLSPLMMAAKTG--------------------------------------- 420
          |||||||||||||||||||||
Db   361  NLEAVLNNDGLSPLMMAAKTG                                         381

Qy   421  LSSLDTCGEEASVLEIILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
                                 ||||||||||||||||||||||||||||||||||||||
Db   382  --------------------KIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC   420

Qy   481  AMVIFTLITAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AMVIFTLITAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 480

Qy   541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  540

Qy   601  TYSIMIQKILFKDLFRPLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TYSIMIQKILFKDLFRPLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  600

Qy   661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVVTYIILTFVLLLNMLIALMGE 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVVTYIILTFVLLLNMLIALMGE 660

Qy   721  TVGQVSKESKHIWKLQ  736
          ||||||||||||||||
Db   661  TVGQVSKESKHIWKLQ  676
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RESULT 4
US-09-235-451-25
; Sequence 25, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 843
; TYPE: PRT
; ORGANISM: chicken
US-09-235-451-25

Query Match       41.6%;   Score 1604.5;   DB 3;   Length 843;
Best Local Similarity   47.5%;   Pred. No. 1.4e-143;
Matches   343;   Conservative   128;   Mismatches   184;   Indels   67;   Gaps   18;

```
Qy    41  EGEDGSLSPSPADASRPAGPGDGRPNLRMKFQGAFRKGVPNPIDLLESTLY--ESSVVPG  98
          |||||                                                 :|:|
Db    27  DGDSAL--ETAD--------------------NLQQTF----SNKVQPSKSNIFARRGRFVMG 64

Qy    99  ---PKKAPMDSLFDY------GTYRHHSSDNKRWRKKIIEKQP--QSPKAPAPQPPPIL  146
             |||:                  :: ::                ::|
Db    65  DCDKDMAPMDSFYQMDHLMAPSVIKFHANMERGKLHKLLSTDSITGCSEKA--------F  116

Qy   147  KVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGR  206
          | :: |:|| :|:|||| ||| ||  |:|   |||::|| | |||||| ||| |||: |
Db   117  KFYDRRRIFDAVARGSTKDLDDLLLLYLNRTLKHLTDDEFKEPETGKTCLLKAMLNLHDGK  176

Qy   207  NDTIPVLLDIAERTGNMREFINSPPRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHA  266
          |||||:|||||: |  ||| ||||  ||| |||||||||||||   | |||||| |||||
Db   177  NDTIPLLLDIAKKTGTLKEFVNAEYTDNYYKGQTALHIAIERRNMYLVKLLVQNGADVHA  236

Qy   267  QARGRFFQP-KDEGGYYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVL   325
           | | |    | ||||:|||||||||||||| :| :: |||| | |           ||
Db   237  RACGEFFRKIKGKPG-FYFGELPLSLAACTNQLCIVKFLLENPYQAADIAAEDSMGNMVL  295

Qy   326  HALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGI  385
          | ||:|||||::|||||||||:: |:   | |   || :|   :  | | | |||||||
Db   296  HTLVEIADNTKDNTKFVTKMYNNILILGAKINPILKLELELTNKKGLTPLTLAAKTGKIGI  355

Qy   386  FQHIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVVNSKIEN   445
          |  | |||    ||||||||  |||||| ||||||| |||  |:||||| | | || |
Db   356  FAYILRREIKDPECRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVLEIIAYSSETPN  414

Qy   446  RHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLE--GTPPYPY-  502
          |||| :||:|: ||:|||  | : |:: ::  :   | | || ||: ::   ::|
Db   415  RHEMLLVEPLNRLLQDKWDRFVKHLFYFNFFVVAIHISILTTAAYRPVQKGDKPPFAFG   474

Qy   503  RTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIV  562
           :  :|  : ||:|::   |||| | |  :    | : :||||| ::::|| : : |:|:
Db   475  HSTGEYFRVTGEIISVLGGLYFFFRGIQ-YFVQRRPSLKTLIVDSYSEVLFFVHSLLLLS  533

Qy   563  SAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYL  622
          | :|| || | | | ||| | || |: ||:|:|  : | ::|| | :||||  ||:|||
Db   534  SVVLYFCGQELYVASMVFSLALGWANMLYYTRGFQQMGYSVMIAKMLRDLCRFMFVYL   593

Qy   623  LFMIGYASALVSLLNPCANMKVCNEDQ-TNCTVPTYPSCRDSETFST------FLLDLF  674
           ::|| : ||| |:::    | ::| :  |  ||: :  : : |:|  ||   ::| |
Db   594  VFLLGFSTAVVTLIED--------DNEGQDTNSS--EYARCSHTKRGRTSVNSLYYTCLELF 645

Qy   675  KLTIGMGDLEMLSSTKYPVVFIILLVVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWK 734
          | |||||||| : :     |:||:||::| || |:|:|||||||||||| :::::| ||| 
Db   646  KFTIGMGDLEFTENYRFKSVFVILLVLLVVILTYILTLLNMLIALMGETVSKIAQESKSIWK 705

Qy   735  LQ 736
          ||
Db   706  LQ 707
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RESULT 5
US-09-978-303-25
; Sequence 25, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25

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; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 838
; TYPE: PRT
; ORGANISM: R. rattus
US-09-235-451-2

Query Match         40.9%;  Score 1579.5;  DB 3;  Pred. No. 3.3e-141;
Best Local Similarity 44.6%;
Matches 338;  Conservative 129;  Mismatches 193;  Indels 97;  Gaps 16;

Qy   16 AELPGDESGTPGGE------------------APPLSSLANLFEGEDGSLSPSPADA   54
Db    5 ASLDSEESSESPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSRTRLF-GKGDSBEASPLDC 63

Qy   55 SRPAGPGDGRPNLRMKFQGAFRKGVPN-PIDLLESTLYESSVVPGPKKAPMDSLFDYGTY  113
Db   64 PYEEG----------------GLASCPIITVSSVL----TIQRPGDGP-------ASV    94

Qy  114 RHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFL  173
Db   95 RPSSQDS------------VSAGEKPP--RLYDRRSIFDAVAQSNCQELESLLPFL      136

Qy  174 LTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRD  233
Db  137 QRSKKRLTDSEFKDPETGKTCLLKAMLNLHNGQNDTIALLLDVARKTDSLKQFVNASYTD  196

Qy  234 IYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAA  293
Db  197 SYYKGQTALHIAIERRNMTLVTLLVENGADVQAAANGDFFKKTKGRPGFYFGELPLSLAA  256

Qy  294 CTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC  353
Db  257 CTNQLAIVKFLLQNSWQPADISARDSVGNTVLHALVEVADNTVDNTKFVTSMYNEILLILG 316

Qy  354 ARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP  413
Db  317 AKLHPTLKLEEITNRKGLTPLALAASSGKIGVLAYIIQREIHEPECRHLSRKFTEWAYGP  376

Qy  414 VYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWKRKFGAVSFY 472
Db  377 VHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFY  435

Qy  473 INVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTV-DYLRLAGEVITLFTGVLFFFTNIKD  531
Db  436 FNFFVYCLYMIFTAAAYRPVEGLLPPYKLKNTVGDYFRVTGEILSVSGGVVFFFRGIQ-   494

Qy  532 LFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALVSLLNPCANMKVCNEDQTN       591
Db  495 YFLQRRPSLKSLFVDSYSEILFFVQSLFMLSVSVVLYFSQRKEYVASMVFSLAMGWTNMLY 554

Qy  592 FTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTN 651
Db  555 YTRGFQQMGIYAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLI----------EDGKN 604

Qy  652 CTVP---TYPSCRDS------------ETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILL 699
Db  605 NSLPMESTPHKCRGSACKPGNSYNSLYST-CLELFKPTIGMGDLEFTENYDFKAVFILL   663

Qy  700 VTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKLQ 736
Db  664 LAYVILTYILLNMLIALMGETVNKIAQESKNIWKLQ  700

RESULT 7
US-09-132-316-3
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; LENGTH: 843
; TYPE: PRT
; ORGANISM: chicken
US-09-978-303-25

Query Match         41.6%;  Score 1604.5;  DB 4;  Length 843;
Best Local Similarity 47.5%;  Pred. No. 1.4e-143;
Matches 343;  Conservative 128;  Mismatches 184;  Indels 67;  Gaps 18;

Qy   41 EGEDGSLSPSPADASRPAGPGDGRPNLRMKFQGAFRKGVPNPIDLLESTLY--ESSVVPG  98
Db   27 DGEDSAL--ETAD----------------NLQGTF----SNKVQPSKSNIFARRGRFVMG  64

Qy   99 ---PKKAPMDSLFDY------GTYRHHSSDNKRWRKKIIEKQP--QSPKAPAQPPPIL   146
Db   65 DCDKDMAPMDSFYQMDHLMAPSVIKFHANMERGKLHKLLSTDSITGCSEKA--------F 116

Qy  147 KVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGR  206
Db  117 KFYDRRRIFDAVARGSTKDLDDLILLYLNRTLKGHLTDDEFKEPETGKTCLLKAMLNLHDGK 176

Qy  207 NDTIPVLLDIAERTGNMREFINSPFRDIYRGQTALHIAIERRCKHYVELLVAQGADVHA   266
Db  177 NDTIPLLLDIAKKTGTLKEFVNAEYTDNYYKGQTALHIAIERRNMYLVKLLVQNGADVHA  236

Qy  267 QARGRFFQP-KDEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVL  325
Db  237 RACGEFPRKIKGKPG-FYFGELPLSLAACTNQLCIVKFLLENPYQAADIAAEDSMGNMVL  295

Qy  326 HALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGI  385
Db  296 HTLVEIADNTKDNTKFVTKMYNNILIGAKINPILKLEELTNKKGLTPLTLAAKTGKIGI   355

Qy  386 FQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVYNSKIEN  445
Db  356 FAYILRREIKDPECRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVLEIIAYSSETPN  414

Qy  446 RHEMLAVEPINELLRDKWKRKFPGAVSFYINVVSYLCAMVIFTLTAYYQPLE--GTPPYPY- 502
Db  415 RHEMLLVEPLNRLLQDKWDRFVKHLFYFNFFVYAIHISILTTAAYYRPVQKGDKPPFAFG  474

Qy  503 RTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIV  562
Db  475 HSTGEYFRVTGEILSVLGGLYFFFRGIQ-YFVQRRPSLKTLIVDSYSEVLFFVHSLLLLS  533

Qy  563 SAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYL  622
Db  534 SVVLYFCGQELYVASMVFSLALGWANMLYYTRGFQQMGIYSVMIAKMILRDLCRFMFVYL  593

Qy  623 LFMIGYASALVSLLNPCANMKVCNEDQ-TNCTVPTYPSCRDSETFST-------FLLDLF  674
Db  594 VFLLGFSTAVVTLIED------DNEGQDTNSS--EYARCSHTKRGTSYNSLYYTCLELF   645

Qy  675 KLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWK  734
Db  646 KFTIGMGDLEFTENYRFKSVFVILLVLYVILTYILLNMLIALMGETVSKIAQESKSIWK   705

Qy  735 LQ 736
Db  706 LQ 707

RESULT 6
US-09-235-451-2
; Sequence 2, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
```

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; Sequence 3, Application US/09132316B
; Patent No. 6444440
; GENERAL INFORMATION:
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1488.1110000
; CURRENT APPLICATION NUMBER: US/09/132,316B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-132-316-3

Query Match         40.9%;    Score 1579.5;  DB 4;   Length 838;
Best Local Similarity 44.6%;  Pred. No. 3.3e-141;
Matches 338;  Conservative 129;  Mismatches 193;  Indels 97;  Gaps 16;

Qy   16 AELPGDESGTPGGE------------------------------AFPLSSLANLFEGEDGSLSPSPADA 54
Db    5 ASLDSEESESSPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSRTRLF-GKGDSEEASPLDC 63

Qy   55 SRPAGPGDGRPNLRMKFQGAFRKGVPN-PIDLLESTLYESSVVPGPKKAPMDSLFDYGTY 113
Db   64 PYEEG-----------GLASCPIITVSSVL----TIQRPGDGP------ASV 94

Qy  114 RHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFL 173
Db   95 RPSSQDS-------------VSAGEKPP--RLYDRRSIFDAVAQSNCQELESLLPFL 136

Qy  174 LTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRD 233
Db  137 QRSKKRLTDSEFKDPETGKTCLLKAMLNLHNGQNDTIALLLDVARKTDSLKQFVNASYTD 196

Qy  234 IYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAA 293
Db  197 SYYKGQTALHIAIERRNMTLVTLLVENGADVQAAANGDFFKKTKGRPGFYFGELPLSLAA 256

Qy  294 CTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC 353
Db  257 CTNQLAIVKFLLQNSWQPADISARDSVGNTVLHALVEVADNTVDNTKFVTSMYNEILILG 316

Qy  354 ARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP 413
Db  317 AKLHPTLKLEEITNRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTEWAYGP 376

Qy  414 VYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSFY 472
Db  377 VHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFY 435

Qy  473 INVVSYLCAMVIFLTAYYQPLEGTPPYYRTTV-DYLRLAGEVITLFTGVLFFFTNIKD 531
Db  436 FNFFVYCLYMIIFTAAAYRPVEGLPYVEGLPPYKLKNTVGDYPRVTGEILSVSGGVVFFFRRGIQ- 494

Qy  495 YPFLQRRPSLKSLFVDSYSEILFFVQSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLY 554
Db  532 LFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALY 591

Qy  555 YTRGFQQMGIYAVMIEKMILRDLCRFMVFYLVFLFGFSTAVVTLI----------EDGKN 604
Db  592 FTRGLKLTGTYSIMIQKILFKDILFRFLLVYLLFMIGYASAALVSLLNPCANMKVCNEDQTN 651

Qy  605 NSLPMESTPHKCRGSACKPGNSYNSLYST-CLELFKFTIGMGDLEFTENYDFKAVFILL 663
Db  652 CTVP---TYPSCRDS-------ETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFILL 699
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; RESULT 8
US-09-667-422-9
; Sequence 9, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Rattus sp.
; PUBLICATION INFORMATION:
; AUTHORS: Caterina, Michael J.
; AUTHORS: Schumacher, Mark A.
; AUTHORS: Tominaga, Makoto
; AUTHORS: Rosen, Tobias A.
; TITLE: The capsaicin receptor: a heat-activated ion channel in
; TITLE: the pain pathway
; JOURNAL: Nature
; VOLUME: 389
; PAGES: 816-824
; DATE: 1997
US-09-667-422-9

Query Match         40.9%;    Score 1579.5;  DB 4;   Length 838;
Best Local Similarity 44.6%;  Pred. No. 3.3e-141;
Matches 338;  Conservative 129;  Mismatches 193;  Indels 97;  Gaps 16;

Qy   16 AELPGDESGTPGGE------------------------------AFPLSSLANLFEGEDGSLSPSPADA 54
Db    5 ASLDSEESESSPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSRTRLF-GKGDSEEASPLDC 63

Qy   55 SRPAGPGDGRPNLRMKFQGAFRKGVPN-PIDLLESTLYESSVVPGPKKAPMDSLFDYGTY 113
Db   64 PYEEG-----------GLASCPIITVSSVL----TIQRPGDGP------ASV 94

Qy  114 RHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFL 173
Db   95 RPSSQDS-------------VSAGEKPP--RLYDRRSIFDAVAQSNCQELESLLPFL 136

Qy  174 LTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRD 233
Db  137 QRSKKRLTDSEFKDPETGKTCLLKAMLNLHNGQNDTIALLLDVARKTDSLKQFVNASYTD 196

Qy  234 IYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAA 293
Db  197 SYYKGQTALHIAIERRNMTLVTLLVENGADVQAAANGDFFKKTKGRPGFYFGELPLSLAA 256

Qy  294 CTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC 353
Db  257 CTNQLAIVKFLLQNSWQPADISARDSVGNTVLHALVEVADNTVDNTKFVTSMYNEILILG 316

Qy  354 ARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP 413
Db  317 AKLHPTLKLEEITNRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTEWAYGP 376

Qy  414 VYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSFY 472
Db  377 VHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFY 435

Qy  473 INVVSYLCAMVIFLTAYYQPLEGTPPYYRTTV-DYLRLAGEVITLFTGVLFFFTNIKD 531
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Qy  700 VTYIILTFVLLNMLIALMGETVGQVSKESKHIWKLQ 736
Db  664 LAVVILTYILLLNMLIALMGETVNKIAQESKNIWKLQ 700
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Db 257 CTNQLAIVKFLLQNSWQPADISARDSVGNTVLHALVEVADNTVDNTKFVTSMYNEILLIG 316

Qy 354 ARLFPDSNLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP 413
       : : :: | : : : : ::| :|||| : :|||||
Db 317 AKLHPTLKLEEITNRKGLHTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTEWAYGP 376

Qy 414 VYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSFY 472
       |:|:||||||:| :||||| :-: |||| : :|
Db 377 VHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFY 435

Qy 473 INVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTV-DYLRLAGEVITLFTGVLFFFTNIKD 531
       : :|| |::: : ||| : | :|:|:
Db 436 FNFFVYCLYMIIFTAAAYRPVEGLPPYKLKNTVGDYFRVTGEILSVSGGVYFFFRGIQ- 494

Qy 532 LFMKKCPGVNSLFIDGSFQLLYFIYSVLIVISVSAALYLAGIEAYLAVMVFALVLGWMNALY 591
       ||||||||||||||:|| :|||| :: | | |:||:|||:||:|||||||||||||||
Db 495 YFLQRRPSLKSLFVDSYSEILFFVQSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLY 554

Qy 592 FTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTN 651
       :|||: :|:|:|:|:||||||| |:|:||||||||:||:||||:::||:|:: :|:
Db 555 YTRGFQOMGIYAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLI----------EDGKN 604

Qy 652 CTVP---TYPSCRDS--------ETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILL 699
       :|| || | :|:|||||| |:||:|||||
Db 605 NSLPMESTPHKCRGSACKPGNSYNSLYST-CLELFKFTIGMGDLEFTENYDFKAVFIILL 663

Qy 700 VTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKLQ 736
       |:||:|:||||||||||||||:: ::||:|:||||||
Db 664 LAYVILTYILLLNMLIALMGETVNKIAQESKNIWKLQ 700

RESULT 10
US-09-197-636-2
; Sequence 2, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID
; APPLICANT: HAYES, PHILIP
; APPLICANT: MEADOWS, HELEN
; APPLICANT: DAVIS, JOHN
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,636
; FILING DATE: 23-NOV-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9805137.8
; FILING DATE: 12-MAR-1998
; APPLICATION NUMBER: UK 9815791.0
; FILING DATE: 21-JUL-1998
; APPLICATION NUMBER: UK 9819278.4
; FILING DATE: 03-SEP-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30075
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169

Db 436 FNFFVYCLYMIIFTAAAYRPVEGLPPYKLKNTVGDYFRVTGEILSVSGGVYFFFRGIQ- 494

Qy 532 LFMKKCPGVNSLFIDGSFQLLYFIYSVLIVISVSAALYLAGIEAYLAVMVFALVLGWMNALY 591

Db 495 YFLQRRPSLKSLFVDSYSEILFFVQSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLY 554

Qy 592 FTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTN 651
       :|||: :|:|:|:|:||||||| |:|:||||||||:||:||||:::||:|:: :|:
Db 555 YTRGFQOMGIYAVMIEKMILRDLCRFMFVYLVFLFGFSTAVVTLI----------EDGKN 604

Qy 652 CTVP---TYPSCRDS--------ETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILL 699
       :|| || | :|:|||||| |:||:|||||
Db 605 NSLPMESTPHKCRGSACKPGNSYNSLYST-CLELFKFTIGMGDLEFTENYDFKAVFIILL 663

Qy 700 VTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKLQ 736
       |:||:|:||||||||||||||:: ::||:|:||||||
Db 664 LAYVILTYILLLNMLIALMGETVNKIAQESKNIWKLQ 700

RESULT 9
US-09-978-303-2
; Sequence 2, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 2
; LENGTH: 838
; TYPE: PRT
; ORGANISM: R. rattus
US-09-978-303-2

Query Match         40.9%;  Score 1579.5; DB 4;  Length 838;
Best Local Similarity  44.6%;  Pred. No. 3.3e-141;
Matches 338;  Conservative 129; Mismatches 193;  Indels 97;  Gaps 16;

Qy  16 AELPGDESGTPGGE----------------AFPLSSLANLFEGEDGSLSPSPADA 54
        : : |: || || ||| || ||
Db   5 ASLDSESESPPQENSCLDPPDRDNCKPPPVKPHIFTTRSRTRLF-GKGDSEEASPLDC 63

Qy  55 SRPAGPGDGRPNLRMKFQGAFRKGVPN-PIDLLESTLYESSVVPGPKKAPMDSLFDYGTV 113
        :|||| :|: |:: :::::|| ::|: | :
Db  64 PYEEG----------------GLASCPIITVSSVL----TIQRPGDGP------ASV 94

Qy 114 RHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFL 173
        | |:: |:| | |||| :| ||
Db  95 RPSSQDS---------------VSAGEKPP--RLYDRRSIFDAVAQSNCQELESLLPFL 136

Qy 174 LTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRD 233
        |||||| :|: | :: ::|||| ::||: |
Db 137 QRSKKRLTDSEFKDPETGKTCLLKAMLNLHNGQNDTIALLLDVARKTDSLKQFVNASYTD 196

Qy 234 IYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAA 293
        |||||||||||||:| :|: :: :||||:|||||: :: ::|||:||||
Db 197 SYYKGQTALHIAIERRNMTLVTLLVENGADVQAAANGDFFKKTKGRPGFYFGELPLSLAA 256

Qy 294 CTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC 353
        |||| ||: ::| | |: :|| :|:|::|: ::|

;  INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH:  839 amino acids
;          TYPE:  amino acid
;          STRANDEDNESS:  single
;          TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-09-197-636-2

Query Match         40.4%;    Score 1557.5;    DB 3;    Length 839;
Best Local Similarity  44.5%;    Pred. No. 4.1e-139;
Matches  321;    Conservative 138;    Mismatches 188;    Indels  74;    Gaps    12;

Qy    49  PSPADASRPAGPGDGRPNL------RMKFQG----AFRKGVPNPIDLLES--TLYESSV  95
              : ::|||: :|||  | ||   || ||     :| :|
Db    22  PDPLDGDPNSRPPAKPQLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV  81

Qy    96  V------PGPKKAPMDSLFDYGTYRHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVF  149
              |:
Db    82  ITIQRPGDGPTGARL----------------------LSQDSVAASTEKTLRLY  113

Qy   150  NRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT  209
              : :| :|: :::||  |||||:  :|:|
Db   114  DRRSIFEAVAQNNCQDLESLLLFLFQKSKKHLTDNEFKDPETGKTCLLKAMLNLHDGQNTT  173

Qy   210  IPVLLDIAERTGNMREFINSPFRDIYRGQTALHIAERRCKHYVELLVAQGADVHAQAR  269
              |||||||||||||  |||  || ||||||||||||| :| |||||||||||
Db   174  IPLLLEIARQTDSLKELVNASYTDSYYKGQTALHIAIERRNNMALVTLLVENGADVQAAAH  233

Qy   270  GRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALV  329
              |:||||| ::||||||||||||||| :| :| |||||| ||:|
Db   234  GDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHALV  293

Qy   330  AIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHI  389
              ||||||| |||||||  :| ||::|| :| | ||||||||
Db   294  EVADNTADNTKFVTSMYNEILLGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVLAYI  353

Qy   390  IRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVY--NSKIENRHE  448
              ||||||||||||||:|:||  || :||||||||||||||||||||||||
Db   390  IRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVY--NSKIENRHE  448

Qy   449  MLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYRTTVDY  508
              ||||||:|:|| |||| | | :|| |:|:|
Db   413  MLLVEPLNRLLQDKWDRFVKRIFYFNFLVYCLYMIFTMAAAYYRPVDGLPPFKMEKTGDY  472

Qy   509  LRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFPIDGSFQLLYFIYSVLVIVSAALYL  568
              : | ||| |||| : ||| :: :|:| : ||  |
Db   473  FRVTGEILSVLGGVVYFFFRGIQ-YFLQRRPSMKTLFVDSYSEMLFPLQSLFMLATVVLYF  531

Qy   569  AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGY  628
              |||||  :|| |:| || | : |  ::||||| ||
Db   532  SHLKEYVASMVFSLALGWTNMLYYTRGFQQOMGIYAVMIEKMILRDLCRFMFYYIVFLFGF  591

Qy   629  ASALVSLLNPCANMKVCNEDQTNCTVPTY------PSCRDSET----FSTFLLDLFK  675
              ||| || :|     |      ||||
Db   592  STAVVTLI---------EDGKNDSLPSESTSHRWRGPACRPPDSSYNSLYST-CLELFK  640

Qy   676  LTIGMGDLEMLSSTKYPVVFIILLVTVIILITFVLLNMLIALMGETVGQVSKESKHIWKL  735
              |||||||| || |||| ||||||||||||||| :|:|||||| |||
Db   641  FTIGMGDLEFTENYDFKAVFIILLAYVILTYILLLAVFILLLNMLIALMGETVNKIAQESKNIWKL  700

Qy   736  Q  736
Db   701  Q  701

RESULT 11
US-09-197-636-8
;  Sequence 8, Application US/0197636
;  Patent No. 6239267
;  GENERAL INFORMATION:
;      APPLICANT: DUCKWORTH, DAVID
;      APPLICANT: HAYES, PHILIP

---

;  APPLICANT: MEADOWS, HELEN
;  APPLICANT: DAVIS, JOHN
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  NUMBER OF SEQUENCES: 8
;  CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Ratner & Prestia
;      STREET: P.O. Box 980
;      CITY: Valley Forge
;      STATE: PA
;      COUNTRY: US
;      ZIP: 19482-0980
;  COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ for Windows Version 2.0
;  CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/197,636
;      FILING DATE: 23-NOV-1998
;      CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: UK 9805137.8
;      FILING DATE: 12-MAR-1998
;      APPLICATION NUMBER: UK 9815791.0
;      FILING DATE: 21-JUL-1998
;      APPLICATION NUMBER: UK 9819278.4
;      FILING DATE: 03-SEP-1998
;  ATTORNEY/AGENT INFORMATION:
;      NAME: Prestia, Paul F
;      REGISTRATION NUMBER: 23,031
;      REFERENCE/DOCKET NUMBER: GP-30075
;  TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 601-407-0700
;      TELEFAX: 610-407-0701
;      TELEX: 846169
;  INFORMATION FOR SEQ ID NO: 8:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 839 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-09-197-636-8

Query Match         40.3%;    Score 1556.5;    DB 3;    Length 839;
Best Local Similarity  44.5%;    Pred. No. 5.1e-139;
Matches  321;    Conservative 138;    Mismatches 188;    Indels  74;    Gaps    12;

Qy    49  PSPADASRPAGPGDGRPNL------RMKFQG----AFRKGVPNPIDLLES--TLYESSV  95
              : ::|||: :|||  | ||   || ||     :| :|
Db    22  PDPLDGDPNSRPPAKPQLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV  81

Qy    96  V------PGPKKAPMDSLFDYGTYRHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVF  149
              |:
Db    82  ITIQRPGDGPTGARL----------------------LSQDSVAASTEKTLRLY  113

Qy   150  NRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT  209
              : :| :|: :::||  |||||:  :|:|
Db   114  DRRSIFEAVAQNNCQDLESLLLFLFQKSKKHLTDNEFKDPETGKTCLLKAMLNLHDGQNTT  173

Qy   210  IPVLLDIAERTGNMREFINSPFRDIYRGQTALHIAERRCKHYVELLVAQGADVHAQAR  269
              |||||||||||||  |||  || ||||||||||||| :| |||||||||||
Db   174  IPLLLEIARQTDSLKELVNASYTDSYYKGQTALHIAIERRNNMALVTLLVENGADVQAAAH  233

Qy   270  GRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALV  329
              |:||||| ::||||||||||||||| :| :| |||||| ||:|
Db   234  GDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHALV  293

Qy   330  AIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHI  389
              ||||||| |||||||  :| ||::|| :| | ||||||||
Db   294  EVADNTADNTKFVTSMYNEILLGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVLAYI  353

Qy   390  IRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHE  448

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Db  354 LQREIQEPECRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412
Qy  449 MLAVEPINELLRDKWRKFPGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTVDY 508
Db  413 MLIVEPLNRLLQDKWDRFVKRIFYFNFLVYCLYMIIFTMAAYYRPVDGLPPFKMEKTGDY 472
Qy  509 LRLAGEVITLFTGVLFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYL 568
Db  473 FRVTGEILSVLGGVYFFRGIQ-YFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVLYF 531
Qy  569 AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGY 628
Db  532 SHLKEYVASMVFSLALGWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVYVVFLFGF 591
Qy  629 ASALVSLLNPCANMKVCNEDQTNCTVPTY--------PSCRDSET-----FSTFLLDLFK 675
Db  592 STAVVTLI---------EDGKNDSLPSESTSHRWGPACRPPDSSYNSLYST-CLELFK 640
Qy  676 LTIGMGDLEMLSSTKYPVVFEIILLVVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKL 735
Db  641 FTIGMGDLEFTENYDFKAVFIILLLAVVILTYILLLNMLIALMGETVNKIAQESKNIWKL 700
Qy  736 Q 736
Db  701 Q 701
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RESULT 12
US-09-235-451-34
; Sequence 34, Application US/09235451
; GENERAL INFORMATION:
;   APPLICANT: Julius, David J.
;   APPLICANT: Caterina, Michael J.
;   APPLICANT: Brake, Anthony J.
;   TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
;   TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
;   TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
;   FILE REFERENCE: 9076/084CIP
;   CURRENT APPLICATION NUMBER: US/09/235,451
;   CURRENT FILING DATE: 1999-01-22
;   PRIOR APPLICATION NUMBER: 60/072,151
;   PRIOR FILING DATE: 1998-01-22
;   PRIOR APPLICATION NUMBER: 08/915,461
;   PRIOR FILING DATE: 1997-08-20
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
;   LENGTH: 839
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-235-451-34

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Query Match             40.3%;  Score 1556.5;  DB 3;  Length 839;
Best Local Similarity   44.5%;  Pred. No. 5.1e-139;
Matches   321;  Conservative   138;  Mismatches   188;  Indels   74;  Gaps   12;

Qy   49 PSPADASRPAGPGDGRPNL------RMKFQG-----AFRKGVPNPIDLLES--TLYESSV 95
Db   22 PDPLDGDPNSRPPAKPQLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV 81
Qy   96 V------PGPKKQAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVF 149
Db   82 ITIQRPGDGPTGARL----------------------------LSQDSVAASTEKTLRLY 113
Qy  150 NRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEBFREPSFGKTCLPKALLNLSNGRNDT 209
Db  114 DRRSIFEAVAQNNCQDLESLLLFLQKSKKHLTDNEFKDPETGKTCLLKAMLNLHDGQNTT 173
Qy  210 IPVLLDIAERTGNMREFINSPFRDIYRGQTALHIAIERRCKHYVELLVAQGADVHAQAR 269
Db  174 IPLLLEIARQTDSLKELVNASYTDSYKGQTALHIAIERRNMALVTLLVENGADVQAAAH 233
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Db  234 GDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHALV 293
Qy  270 GRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALV 329
Db  294 EVADNTADNTKFVTSMYNEILILGAKLHPTLKEELTNKKGMTPLALAAGTGKIGVLAYI 353
Qy  330 AIADNTRENTKFVTKMYDLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHI 389
Db  354 LQREIQEPECRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412
Qy  390 IRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHE 448
Db  413 MLIVEPLNRLLQDKWDRFVKRIFYFNFLVYCLYMIIFTMAAYYRPVDGLPPFKMEKTGDY 472
Qy  449 MLAVEPINELLRDKWRKFPGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTVDY 508
Db  473 FRVTGEILSVLGGVYFFRGIQ-YFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVLYF 531
Qy  509 LRLAGEVITLFTGVLFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYL 568
Db  532 SHLKEYVASMVFSLALGWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVYVVFLFGF 591
Qy  569 AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGY 628
Db  592 STAVVTLI---------EDGKNDSLPSESTSHRWGPACRPPDSSYNSLYST-CLELFK 640
Qy  629 ASALVSLLNPCANMKVCNEDQTNCTVPTY--------PSCRDSET-----FSTFLLDLFK 675
Db  641 FTIGMGDLEFTENYDFKAVFIILLLAVVILTYILLLNMLIALMGETVNKIAQESKNIWKL 700
Qy  676 LTIGMGDLEMLSSTKYPVVFEIILLVVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKL 735
Db  701 Q 701
Qy  736 Q 736
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RESULT 13
US-09-978-303-34
; Sequence 34, Application US/0997303
; Patent No. 6790629
; GENERAL INFORMATION:
;   APPLICANT: Julius, David J.
;   APPLICANT: Caterina, Michael J.
;   APPLICANT: Brake, Anthony J.
;   TITLE OF INVENTION: Nucleic acid sequences encoding
;   TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
;   TITLE OF INVENTION: polypeptides and uses thereof
;   FILE REFERENCE: UCAL084CON
;   CURRENT APPLICATION NUMBER: US/09/978,303
;   CURRENT FILING DATE: 2001-10-15
;   PRIOR APPLICATION NUMBER: 09/235,451
;   PRIOR FILING DATE: 1999-01-22
;   PRIOR APPLICATION NUMBER: 60/072,151
;   PRIOR FILING DATE: 1998-01-22
;   PRIOR APPLICATION NUMBER: 08/915,461
;   PRIOR FILING DATE: 1997-08-20
;   NUMBER OF SEQ ID NOS: 48
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 839
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-303-34

```
Query Match             40.3%;  Score 1556.5;  DB 4;  Length 839;
Best Local Similarity   44.5%;  Pred. No. 5.1e-139;
Matches   321;  Conservative   138;  Mismatches   188;  Indels   74;  Gaps   12;

Qy   49 PSPADASRPAGPGDGRPNL------RMKFQG-----AFRKGVPNPIDLLES--TLYESSV 95
Db   22 PDPLDGDPNSRPPAKPQLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV 81
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Qy   96 V------PGPKKAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVF 149
        :       ||:|                                        |:|:|
Db   82 ITIQRPGDGPTGARL----------------------------------LSQDSVAASTEKTLRLY 113

Qy  150 NRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT 209
        |:|||||:  :: ||:::||||:|||:|:|
Db  114 DRRSIFEAVAQNNCQDLESLLLFLQKSKGHLTDNEFKDPETGKTCLLKAMLNLHDGQNTT 173

Qy  210 IPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQAR 269
        |:|||||| || :|: :|||:|||| |:::|:||||||||||||||||
Db  174 IPLLLEIARQTDSLKELVNASYTDSYYKGQTALHIAIERRNMALVTLLVENGADVQAAAH 233

Qy  270 GRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNLTENPHKKADMRRQDSRGNTVLHALV 329
        ||||||:|||||||||||||||:|: :||||||| :|: |||||||||||||
Db  234 GDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHALV 293

Qy  330 AIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHI 389
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Db  294 EVADNTADNTKFVTSMYNEILILGAKLHPTLKEELTNKKGMPLALAAGTGKIGVLAYI 353

Qy  390 IRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHE 448
        ::|||:| |||:|||:|: ||: ::|:|||||||:|::
Db  354 LQRBIQEPBCRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412

Qy  449 MLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTVDY 508
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Db  413 MLLVEPLNRLLQDKWDRFVKRIFYFNFLVYCLYMIIFTMAAYYRPVDGLPPFKMEKTGDY 472

Qy  509 LRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYL 568
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Db  473 FRVTGEILSVLGGVYFFFRGIQ-YFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVLYF 531

Qy  569 AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGY 628
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Db  532 SHLKEYVASMVFSLALGWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVYVVFLFGF 591

Qy  629 ASALVSLLNPCANMKVCNEDQTNCTVPTY--------PSCRDSET-----FSTFLLDLFK 675
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Qy  676 LTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGETVGQVSKESKHIWKL 735
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Db  641 FTIGMGDLEFTENYDFKAVFIIILLAYVILTYILLLNMLIALMGETVNKIAQESKNIWKL 700

Qy  736 Q 736
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Db  701 Q 701
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RESULT 14
US-09-533-220A-2
; Sequence 2, Application US/09533220A
; Patent No. 6406908
; GENERAL INFORMATION:
; APPLICANT: McIntyre, Peter
; APPLICANT: James, Iain Fraser
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/09/533,220A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30
;
; SEQ ID NO 2
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-220A-2

Query Match       40.3%;  Score 1555.5; DB 4;  Length 839;
Best Local Similarity  44.5%;  Pred. No. 6.4e-139;
Matches 321;  Conservative 137;  Mismatches 189;  Indels  74;  Gaps 12;

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Qy   96 V------PGPKKAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVF 149
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Qy  150 NRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT 209
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Qy  210 IPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQAR 269
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Db  174 IPLLLEIARQTDSLKELVNASYTDSYYKGQTALHIAIERRNMALVTLLVENGADVQAAAH 233

Qy  270 GRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNLTENPHKKADMRRQDSRGNTVLHALV 329
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Db  234 GDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHALV 293

Qy  330 AIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHI 389
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Db  294 EVADNTADNTKFVTSMYNEILILGAKLHPTLKEELTNKKGMPLALAAGTGKIGVLAYI 353

Qy  390 IRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHE 448
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Db  354 LQRBIQEPBCRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412

Qy  449 MLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTVDY 508
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Qy  509 LRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYL 568
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Qy  629 ASALVSLLNPCANMKVCNEDQTNCTVPTY--------PSCRDSET-----FSTFLLDLFK 675
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Db  592 STAVVTLI-----------EDGKNDSLPSESTSHRWRGPACRPPDSSYNSLYST-CLELFK 640

Qy  676 LTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGETVGQVSKESKHIWKL 735
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Db  641 FTIGMGDLEFTENYDFKAVFIIILLAYVILTYILLLNMLIALMGETVNKIAQESKNIWKL 700

Qy  736 Q 736
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Db  701 Q 701
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RESULT 15
US-09-949-016-6937
; Sequence 6937, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 6937
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6937

Query Match         40.3%;   Score 1555.5;  DB 4;  Length 839;
Best Local Similarity   44.5%;  Pred. No. 6.4e-139;
Matches  321;  Conservative 137;  Mismatches 189;  Indels  74;  Gaps  12;

Qy    49  PSPADASRPAGPGDGRPNL-----RMKFQG------AFRKGVPNPIDLLES--TLYESSV  95
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Qy    96  V------PGPKKAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSFKAPAPQPPPILKVF  149
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Db    82  ITIQRPGDGPTGARL-------------------------LSQDSVAASTEKTLRLY  113

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Qy   210  IPVLLDIAERTGNMREFINSPFRDIYRGQTALHIAIERRCKHYVELLVAQGADVHAQAR  269
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Qy   270  GRFFQPKDEGGYFYFGELPLSLAACNQPHIVNYLTENPHKKCADMRRQDSRGNTVLHALV  329
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Db   294  EVADNTADNTKFVTSMYNEILILGAKLHPTLKLEELTNKKGMPLALAAGTGKIGVLAYI  353

Qy   390  IRREVTDEDTRHLSRKFKDWAYGPVVSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHE  448
              | :|    ||||||  |:    : : |:  |: |: :|| :|:|||||  | :||:|:
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Qy   449  MLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVLFTLTAYYQPLEGTPPYPYRTTVDY  508
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Qy   509  LRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFPIDGSFQLLYFIYSVLVIVSAALYL  568
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Db   473  FRVTGEILSVLGGVYFFFRGIQ-YFLQRRPSMKTLFVDSYSEMLFLQSLFMLAITVVLYF  531

Qy   569  AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGY  628
              ::|:| :|: |  :|| |||| | ||     |::  ::  : |: :  |:: : |: |
Db   532  SHLKEYVASMVFSLAIGWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVYIVFLFGF  591

Qy   629  ASALVSLLNPCANMKVCNEDQTNCTVPTY-------PSCRDSET----FSTFLLDLFK  675
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Qy   676  LTIGMGDLEMLSSTKYPVVFILLLVTYIILTFVLLNMLIALMGETVGQVSKESKHIWKL  735
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Db   641  FTIGMGDLEFTENYDFKAVFIILLLLAYVIILTYILLLNMLIALMGETVNKIAQESKNIWKL  700

Qy   736  Q  736
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Db   701  Q  701
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Search completed: May  4, 2005, 22:24:40
Job time : 47 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:      May  4, 2005, 22:15:29 ; Search time 140 Seconds
                                      (without alignments)
                                      1765.463 Million cell updates/sec

Title:        US-10-090-215-12
Perfect score: 3858
Sequence:     1 MADSSEGPRAGPGEVAELPG..........GQVSKESKHIWKLQSGRRRL 742

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:     1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters:      1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :    Published Applications AA:*
      1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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     20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | 3858 | 100.0 | 14 | 742 | 14 | US-10-090-215-12 | Sequence 12, Appl |
| 2 | 3858 | 100.0 | 17 | 742 | 17 | US-10-985-156-12 | Sequence 12, Appl |
| 3 | 3829 | 99.2 | 15 | 831 | 15 | US-10-342-844-76 | Sequence 76, Appl |
| 4 | 3829 | 99.2 | 16 | 870 | 16 | US-10-761-065-2 | Sequence 2, Appli |
| 5 | 3829 | 99.2 | 10 | 871 | 10 | US-09-870-090-2 | Sequence 2, Appli |
| 6 | 3829 | 99.2 | 14 | 871 | 14 | US-10-000-823-7 | Sequence 7, Appli |
| 7 | 3829 | 99.2 | 14 | 871 | 14 | US-10-171-319-17 | Sequence 17, Appl |
| 8 | 3829 | 99.2 | 15 | 871 | 15 | US-10-342-844-54 | Sequence 54, Appl |
| 9 | 3829 | 99.2 | 15 | 871 | 15 | US-10-342-844-58 | Sequence 58, Appl |
| 10 | 3829 | 99.2 | 15 | 871 | 15 | US-10-342-844-78 | Sequence 78, Appl |
| 11 | 3829 | 99.2 | 16 | 871 | 16 | US-10-415-570A-2 | Sequence 2, Appli |
| 12 | 3828 | 99.2 | 14 | 871 | 14 | US-10-027-828-2 | Sequence 2, Appli |
| 13 | 3828 | 99.2 | 15 | 871 | 15 | US-10-342-844-60 | Sequence 60, Appl |

| | | | | | ID | Description |
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| 14 | 3825 | 99.1 | 871 | 14 | US-10-027-828-4 | Sequence 4, Appli |
| 15 | 3823 | 99.1 | 871 | 14 | US-10-090-215-7 | Sequence 7, Appli |
| 16 | 3823 | 99.1 | 871 | 17 | US-10-985-156-7 | Sequence 7, Appli |
| 17 | 3810 | 98.8 | 963 | 10 | US-09-932-165-1477 | Sequence 1477, Ap |
| 18 | 3809 | 98.7 | 871 | 14 | US-10-227-255A-3 | Sequence 3, Appli |
| 19 | 3695 | 95.8 | 871 | 15 | US-10-342-844-84 | Sequence 84, Appli |
| 20 | 3693 | 95.7 | 830 | 14 | US-10-027-828-6 | Sequence 6, Appli |
| 21 | 3693 | 95.7 | 871 | 14 | US-10-027-828-11 | Sequence 11, Appl |
| 22 | 3693 | 95.7 | 871 | 15 | US-10-342-844-66 | Sequence 66, Appl |
| 23 | 3689 | 95.6 | 871 | 15 | US-10-342-844-80 | Sequence 80, Appl |
| 24 | 3687 | 95.6 | 871 | 14 | US-10-027-828-10 | Sequence 10, Appl |
| 25 | 3686 | 95.5 | 871 | 14 | US-10-027-828-8 | Sequence 8, Appli |
| 26 | 3686 | 95.5 | 871 | 14 | US-10-027-828-9 | Sequence 9, Appli |
| 27 | 3685 | 95.5 | 871 | 14 | US-10-171-319-14 | Sequence 14, Appl |
| 28 | 3681 | 95.4 | 871 | 14 | US-10-227-255A-1 | Sequence 1, Appli |
| 29 | 3652 | 94.7 | 870 | 14 | US-10-027-828-13 | Sequence 13, Appl |
| 30 | 3636 | 94.2 | 873 | 15 | US-10-342-844-64 | Sequence 64, Appl |
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| 34 | 3467 | 89.9 | 792 | 9 | US-09-764-367A-2 | Sequence 2, Appli |
| 35 | 3457 | 89.6 | 803 | 9 | US-09-764-367A-8 | Sequence 8, Appli |
| 36 | 3389 | 87.8 | 803 | 15 | US-10-342-844-62 | Sequence 62, Appl |
| 37 | 3284 | 85.1 | 852 | 14 | US-10-027-828-15 | Sequence 15, Appl |
| 38 | 3284 | 85.1 | 852 | 15 | US-10-342-844-36 | Sequence 36, Appl |
| 39 | 3120 | 80.9 | 743 | 9 | US-09-764-367A-11 | Sequence 11, Appl |
| 40 | 3044.5 | 78.9 | 734 | 9 | US-09-764-367A-4 | Sequence 4, Appli |
| 41 | 2847 | 73.8 | 625 | 10 | US-09-932-165-1507 | Sequence 1507, Ap |
| 42 | 2782 | 72.1 | 625 | 10 | US-09-932-165-1506 | Sequence 1506, Ap |
| 43 | 2373.5 | 61.5 | 602 | 10 | US-10-870-090-4 | Sequence 4, Appli |
| 44 | 2373.5 | 61.5 | 602 | 16 | US-10-761-065-4 | Sequence 4, Appli |
| 45 | 2156.5 | 55.9 | 559 | 15 | US-10-297-022-10 | Sequence 10, Appl |

ALIGNMENTS

RESULT 1
US-10-090-215-12
; Sequence 12, Application US/10090215
; Publication No. US2003032097A1
; GENERAL INFORMATION:
;  APPLICANT: Dubin, Adrienne E
;  APPLICANT: Huvar, Arne
;  APPLICANT: Erlander, Mark G
;  APPLICANT: Glass, Charles A
;  TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor
;  TITLE OF INVENTION: VR3
;  FILE REFERENCE: Human VR3 receptors
;  CURRENT APPLICATION NUMBER: US/10/090,215
;  CURRENT FILING DATE:  2002-03-04
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 12
;  LENGTH: 742
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-090-215-12

Query Match             100.0%;  Score 3858;  DB 14;  Length 742;
Best Local Similarity   100.0%;  Pred. No. 9.8e-308;
Matches  742;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
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Db     61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy    121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
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Qy  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
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Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
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Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRFLLVYILFLILTFVLLLNMLIALMGE 660
         ||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYILFLILTFVLLLNMLIALMGE 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLLVTYIILTFVLLLNMLIALMGE 720
         ||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLLVTYIILTFVLLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQSGRRRL 742
         ||||||||||||||||||||||
Db  721 TVGQVSKESKHIWKLQSGRRRL 742
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Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Db  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRFLLVYILFLILTFVLLLNMLIALMGE 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLLVTYIILTFVLLLNMLIALMGE 720
         ||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLLVTYIILTFVLLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQSGRRRL 742
         ||||||||||||||||||||||
Db  721 TVGQVSKESKHIWKLQSGRRRL 742
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; LENGTH: 831
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 804, 816
; OTHER INFORMATION: Xaa = Any Amino Acid
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank XP_012261
; DATABASE ENTRY DATE: 2001-10-16
US-10-342-844-76

Query Match      99.2%;     Score 3829;  DB 15;  Length 831;
Best Local Similarity   100.0%;  Pred. No. 2.8e-305;
Matches 736;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYGELPLSLAACTNQPHI 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYGELPLSLAACTNQPHI 300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFTNIKDLFMKKCPGV 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFTNIKDLFMKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQ 736
          ||||||||||||||||
Db  721 TVGQVSKESKHIWKLQ 736

RESULT 4
US-10-761-065-2
; Sequence 2, Application US/10761065
; Publication No. US2004013573A1
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Query Match      99.2%;     Score 3829;  DB 16;  Length 870;
Best Local Similarity   100.0%;  Pred. No. 3e-305;
Matches 736;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYGELPLSLAACTNQPHI 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYGELPLSLAACTNQPHI 300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFTNIKDLFMKKCPGV 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFTNIKDLFMKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQ 736
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Db   721 TVGQVSKESKHIWKLQ 736
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RESULT 5
US-09-870-090-2
; Sequence 2, Application US/09870090
; Publication No. US20030017527A1
; GENERAL INFORMATION:
;   APPLICANT: Pfizer Product Inc.
;   TITLE OF INVENTION: Human Vanilloid Receptor-Like Proteins
;   FILE REFERENCE: PC9979A
;   CURRENT APPLICATION NUMBER: US20030017527A1
;   CURRENT FILING DATE: 2001-05-30
;   PRIOR APPLICATION NUMBER: US 60/208,156
;   PRIOR FILING DATE: 2000-05-31
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn Ver. 2.1
US-09-870-090-2
;   SEQ ID NO 2
;   LENGTH: 871
;   TYPE: PRT
;   ORGANISM: Human
US-09-870-090-2

Query Match             99.2%;  Score 3829;  DB 10;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 3e-305;
Matches   736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy   121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGQT 240

Qy   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy   301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWKRKFGAVSFYINVVSYLC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWKRKFGAVSFYINVVSYLC 420

Qy   421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy   481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy   541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy   601 TYSIMIQKILFKDLFRFLLVLLFEMIGYASALVSLLNPCANMKVCNEDQTNCTVPYPSC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TYSIMIQKILFKDLFRFLLVLLFEMIGYASALVSLLNPCANMKVCNEDQTNCTVPYPSC 660

Qy   661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
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Db   661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   721 TVGQVSKESKHIWKLQ 736
         ||||||||||||||||
Db   721 TVGQVSKESKHIWKLQ 736

RESULT 6
US-10-000-823-7
; Sequence 7, Application US/10000823
; Publication No. US20030027164A1
; GENERAL INFORMATION:
;   APPLICANT: Bristol-Myers Squibb Company
;   TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NO\
;   TITLE OF INVENTION: HUMAN ION CHANNEL EXPRESSED IN SPINAL CORD AND BRAIN
;   FILE REFERENCE: D0109NP
;   CURRENT APPLICATION NUMBER: US/10/000,823
;   CURRENT FILING DATE: 2001-11-30
;   PRIOR APPLICATION NUMBER: 60/250,587
;   PRIOR FILING DATE: 2000-12-01
;   NUMBER OF SEQ ID NOS: 31
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 7
;   LENGTH: 871
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-000-823-7

Query Match             99.2%;  Score 3829;  DB 14;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 3e-305;
Matches   736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy   121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy   301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy   421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy   481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy   541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
```

```
Qy  601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660

Qy  661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE  720

Qy  721  TVGQVSKESKHIWKLQ  736
         ||||||||||||||||
Db  721  TVGQVSKESKHIWKLQ  736
```

RESULT 7
US-10-171-319-17
; Sequence 17, Application US/10171319
; Publication No. US2003015763A1
GENERAL INFORMATION:
APPLICANT: Ardem Patapoutian
APPLICANT: Andrea Peier
APPLICANT: Peter McIntyre
APPLICANT: Stuart Bevan
APPLICANT: Chuanzheng Song
APPLICANT: Pamposh Ganju
TITLE OF INVENTION: VANILLOID RECEPTOR-RELATED NUCLEIC ACIDS
TITLE OF INVENTION: AND POLYPEPTIDES
FILE REFERENCE: 4-32048A
CURRENT APPLICATION NUMBER: US/10/171,319
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/297,835
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/352,914
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/351,238
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/381,086
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/381,739
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-319-17

Query Match 99.2%; Score 3829; DB 14; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60

Qy   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGKKAPMDSLFDYGTYRHHSSDN  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGKKAPMDSLFDYGTYRHHSSDN  120

Qy  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300
```

```
Qy  301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360

Qy  361  NLEAVLNNDGLSPLMAAKTGKIGIFQHIRREVTDEDTRHLSRKFKDWAYGPVVSSLYD   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  NLEAVLNNDGLSPLMAAKTGKIGIFQHIRREVTDEDTRHLSRKFKDWAYGPVVSSLYD   420

Qy  421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480

Qy  481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV  540

Qy  541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600

Qy  601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660

Qy  661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE  720

Qy  721  TVGQVSKESKHIWKLQ  736
         ||||||||||||||||
Db  721  TVGQVSKESKHIWKLQ  736
```

RESULT 8
US-10-342-844-54
; Sequence 54, Application US/10342844
; Publication No. US20040009537A1
GENERAL INFORMATION:
APPLICANT: Roos, Jack
APPLICANT: Stauderman, Kenneth
APPLICANT: Velicelebi, G"n l
TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
FILE REFERENCE: 37481-3307
CURRENT APPLICATION NUMBER: US/10/342,844
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/347,459
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/401,171
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/405,678
PRIOR FILING DATE: 2002-08-20
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank XP_027181
DATABASE ENTRY DATE: 2002-09-01
US-10-342-844-54

Query Match 99.2%; Score 3829; DB 15; Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60

Qy   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGKKAPMDSLFDYGTYRHHSSDN  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGKKAPMDSLFDYGTYRHHSSDN  120
```

## Left column (RESULT 9 alignment, continued)

```
Db  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
Qy  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
Qy  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
Qy  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
Qy  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
Qy  NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
Qy  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
Qy  AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
Qy  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
Qy  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
Qy  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
Qy  TVGQVSKESKHIWKLQ 736
    |||||||||||||||
Db  TVGQVSKESKHIWKLQ 736
```

## Right column (RESULT 10 alignment)

```
Query Match            99.2%;
Best Local Similarity  100.0%;  Pred. No. 3e-305;
Score 3829;  DB 15;  Length 871;
Matches 736;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
Qy 61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
Qy 121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKRL 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKRL 180
Qy 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
Qy 241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
Qy 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
Qy 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
Qy 481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
Qy 541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
Qy 601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
Qy 661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
Qy 721 TVGQVSKESKHIWKLQ 736
       |||||||||||||||
Db 721 TVGQVSKESKHIWKLQ 736
```

RESULT 11
US-10-415-570A-2
; Sequence 2, Application US/10415570A
; Publication No. US20040198649A1
; GENERAL INFORMATION:
;   APPLICANT: Davis, John Beresford
;   APPLICANT: Gunthorpe, Martin James
;   APPLICANT: Egerton, Julie
;   APPLICANT: Smart, Darren
;   TITLE OF INVENTION: New Use
;   FILE REFERENCE: P32689
;   CURRENT APPLICATION NUMBER: US/10/415,570A
;   CURRENT FILING DATE:  2003-04-23
;   PRIOR APPLICATION NUMBER: PCT/GB01/04739
;   PRIOR APPLICATION FILING DATE: 2001-10-25
;   PRIOR APPLICATION NUMBER: GB 0026114.9
;   PRIOR FILING DATE: 2000-10-25
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 871
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-415-570A-2

Query Match           99.2%;  Score 3829;  DB 16;  Length 871;
Best Local Similarity 100.0%; Pred. No. 3e-305;
Matches 736;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy   121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy   301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVVSYLC 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVVSYLC 420

Qy   421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy   481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy   541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy   601 TYSIMIQKILFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660

Db   601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660

Qy   661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE   720

Qy   721  TVGQVSKESKHIWKLQ  736
          ||||||||||||||||
Db   721  TVGQVSKESKHIWKLQ  736

RESULT 12
US-10-027-828-2
; Sequence 2, Application US/10027828
; Publication No. US2003013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS E
; TITLE OF INVENTION: IT, AND USES THEREOF
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-828-2

Query Match        99.2%;  Score 3828;  DB 14;  Length 871;
Best Local Similarity  99.9%;  Pred. No. 3.7e-305;
Matches  735;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60

Qy   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120

Qy  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300

Qy  301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360

Qy  361  NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420
         |||||||||||||||||||||||| :||||||||||||||||||||||||||||||||||
Db  361  NLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420

Qy  421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480

Qy  481  AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV   540

Db   481  AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV   540

Qy   541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600

Qy   601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660

Qy   661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE   720

Qy   721  TVGQVSKESKHIWKLQ  736
          ||||||||||||||||
Db   721  TVGQVSKESKHIWKLQ  736

RESULT 13
US-10-342-844-60
; Sequence 60, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G"n`l
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAG28029
; DATABASE ENTRY DATE: 2000-10-31
US-10-342-844-60

Query Match        99.2%;  Score 3828;  DB 15;  Length 871;
Best Local Similarity  99.9%;  Pred. No. 3.7e-305;
Matches  735;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60

Qy   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120

Qy  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300

## Left column

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Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQ 736
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Db  721 TVGQVSKESKHIWKLQ 736
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RESULT 14
US-10-027-828-4
; Sequence 4, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS E
; TITLE OF INVENTION: IT, AND USES THEREOF
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-828-4

Query Match 99.1%; Score 3825; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 6.4e-305;
Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
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Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHSSDN 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHSSDN 120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
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## Right column

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Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYPGELPLSLAACTNQPHI 300
        |||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  241 ALHIVIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQ 736
        ||||||||||||||||
Db  721 TVGQVSKESKHIWKLQ 736
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RESULT 15
US-10-090-215-7
; Sequence 7, Application US/10090215
; Publication No. US20030032097A1
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; TITLE OF INVENTION: VR3
; FILE REFERENCE: Human VR3 receptors
; CURRENT APPLICATION NUMBER: US/10/090,215
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-215-7

Query Match 99.1%; Score 3823; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 9.4e-305;
Matches 735; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

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Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
        ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGKKAPRKGVPNPIDLLESTLYESSVVPGKKAPMDSLFDYGTYRHSSDN 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGKKAPMDSLFDYGTYRHSSDN 120
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Db       61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy      121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy      181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy      241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy      301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy      361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy      421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy      481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFTNIKDLFMKKCPGV 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFITNIKDLFMKKCPGV 540

Qy      541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGMWNALYFTRGLKLTG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGMWNALYFTRGLKLTG 600

Qy      601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy      661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720

Qy      721 TVGQVSKESKHIWKLQ 736
            ||||||||||||||||
Db      721 TVGQVSKESKHIWKLQ 736
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Search completed: May  4, 2005, 22:28:03
Job time : 143 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:     May  4, 2005, 22:08:03 ; Search time 21 Seconds
                                (without alignments)
                           3399.659 Million cell updates/sec

Title:      US-10-090-215-12
Perfect score: 3858
Sequence:   1 MADSSEGPRAGPEGEVAELPG..........GQVSKESKHIWKLQSGRRRL 742

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:        283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR 79:*
            1:  _pir1:*
            2:  pir2:*
            3:  pir3:*
            4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1579.5 | 40.9 | 838 | 2 | T09054 | capsaicin receptor |
| 2 | 1551.5 | 40.2 | 839 | 2 | JC7621 | capsaicin receptor |
| 3 | 736.5 | 19.1 | 727 | 2 | JC7796 | epithelial calcium |
| 4 | 724.5 | 18.8 | 725 | 2 | JC7531 | calcium transport |
| 5 | 719 | 18.6 | 723 | 2 | JC7795 | epithelial calcium |
| 6 | 473.5 | 12.3 | 937 | 2 | T37241 | olfactory channel |
| 7 | 473.5 | 12.3 | 957 | 2 | D88651 | protein B0212.5 [i |
| 8 | 435.5 | 11.3 | 900 | 2 | T33026 | hypothetical prote |
| 9 | 313.5 | 8.1 | 790 | 2 | T20312 | hypothetical prote |
| 10 | 278 | 7.2 | 519 | 2 | T24772 | hypothetical prote |
| 11 | 204.5 | 5.3 | 1188 | 2 | T19552 | trp3 protein - rat |
| 12 | 188 | 4.9 | 828 | 2 | JC5807 | calmodulin-binding |
| 13 | 145.5 | 3.8 | 1124 | 2 | JH0588 | TRPC1 protein - hu |
| 14 | 138.5 | 3.6 | 810 | 2 | I38361 | hypothetical prote |
| 15 | 137 | 3.6 | 616 | 2 | T00894 | sodium channel alp |
| 16 | 137 | 3.6 | 1765 | 2 | T42388 | hypothetical prote |
| 17 | 136.5 | 3.5 | 683 | 2 | A85044 | Notch homolog prot |
| 18 | 136 | 3.5 | 2352 | 2 | T30201 | trp protein - frui |
| 19 | 134 | 3.5 | 1275 | 2 | JU0092 | hypothetical prote |
| 20 | 133 | 3.4 | 481 | 2 | T23729 | trp protein - frui |
| 21 | 132 | 3.4 | 1274 | 2 | JN0015 | hypothetical prote |
| 22 | 131.5 | 3.4 | 642 | 2 | S58154 | hypothetical prote |
| 23 | 130.5 | 3.4 | 652 | 2 | D85044 | hypothetical prote |
| 24 | 129.5 | 3.4 | 608 | 2 | G02640 | polycystic kidney |
| 25 | 129 | 3.3 | 823 | 2 | S44873 | ZC21.2 protein - C |
| 26 | 127.5 | 3.3 | 4377 | 2 | A55575 | ankyrin 3, long sp |
| 27 | 126.5 | 3.3 | 643 | 2 | D86167 | protein F21B7.27 [ |
| 28 | 126.5 | 3.3 | 2471 | 2 | A49128 | cell-fate determin |
| 29 | 126 | 3.3 | 2212 | 2 | A41098 | calcium channel pr |
| 30 | 125.5 | 3.3 | 934 | 1 | H71274 | probable ankyrin - |
| 31 | 125.5 | 3.3 | 2529 | 2 | B64635 | toxin-like outer m |
| 32 | 125 | 3.2 | 1957 | 2 | S68453 | sodium channel pro |
| 33 | 124 | 3.2 | 793 | 2 | S68238 | trp-1 protein - hu |
| 34 | 123.5 | 3.2 | 968 | 2 | A37867 | transcription fact |
| 35 | 123 | 3.2 | 751 | 2 | F85043 | hypothetical prote |
| 36 | 123 | 3.2 | 2531 | 2 | T31070 | notch homolog - se |
| 37 | 121 | 3.1 | 488 | 2 | JC7995 | transient receptor |
| 38 | 121 | 3.1 | 1549 | 2 | T13940 | ankyrin - fruit fl |
| 39 | 120.5 | 3.1 | 397 | 2 | T46445 | hypothetical prote |
| 40 | 120.5 | 3.1 | 573 | 2 | D86464 | F12G12.13 protein |
| 41 | 120.5 | 3.1 | 664 | 2 | A56695 | notch2 protein hom |
| 42 | 120 | 3.1 | 633 | 2 | T27499 | hypothetical prote |
| 43 | 119.5 | 3.1 | 574 | 2 | T47566 | hypothetical prote |
| 44 | 119 | 3.1 | 1765 | 2 | T42714 | ankyrin 3, splice |
| 45 | 119 | 3.1 | 1940 | 2 | T42715 | ankyrin 3, splice |

ALIGNMENTS

```
RESULT 1
T09054
capsaicin receptor - rat
N;Alternate names: vanilloid receptor subtype 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accesion: T09054
R;Caterina, M.J.; Schumacher, M.A.; Tominaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D.
Nature 389, 816-824, 1997
A;Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.
A;Reference number: Z16539; MUID:98007969; PMID:9349813
A;Accession: T09054
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-838 <CAT>
A;Cross-references: UNIPROT:O35433; EMBL:AF029310; NID:g2570932; PIDN:AAC53398.1; PID:g2!
A;Experimental source: dorsal root ganglion
C;Keywords: ion channel; receptor

Query Match      40.9%;  Score 1579.5;  DB 2;  Length 838;
Best Local Similarity  44.6%;  Pred. No. 1.1e-103;
Matches  338;  Conservative 129;  Mismatches 193;  Indels 97;  Gaps 16;

Qy     16  AELPGDESGTPGGE----------------------AFPLSSLANLFEGEDGSLSPSPADA  54
               |:|  |||    :                 |||||| |||| ||:||:: |:  ||
Db      5  ASLDSEESSESPPQENSCLDPPDRDPNCKPPPVKPHIFTTRSRTRLF-GKGDSEEASPLDC  63

Qy     55  SRPAGPGDGRPNLRMKFQGAFRKGVPN-PIDLLESTLYESSVVPGPKKAPMDSLFDYGTY  113
               : :  || | ::| :        :      ||::|:::||  : |:
Db     64  PYEEG-----------GLASCPIITVSSVL----TIQRPGDGP----------ASV  94

Qy    114  RHHSSDNKRWRKKIIEKQPSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFL 173
                | :|  ::| ::|::  |  :|  |    ||||| |  :::| ::| ||:||:||
Db     95  RPSSQDS----------------VSAGEKPP--RLYDRRSIFDAVAQSNCQELESLLPFL  136

Qy    174  LTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRD  233
               |||||| :::|   ||| ||  ::| |:|||  :|||||||||:|||:|::|  ||:
Db    137  QRSKKRLTDSEFKDPETGKTCLLKAMLNLHNGQNDTIALLLDVARKTDSLKQFVNASYTD  196

Qy    234  IYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAA  293
               :||||||||||| |||:|||||||:||||| ||  :|::| :| ||||||:|||| ||
Db    197  SYYKGQTALHIAIERRNMTLVTLLVENGADVQAAANGDFKKTKGRPGFYFGELPLSLAA  256

Qy    294  CTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKC  353
               |||:  :|  :::| : |   |:|:|||||||:|||| ||:|||:||||  ::|:|:|
Db    257  CTNQLAIVKFLLQNSWQPADISARDSVGNTVLHALVEVADNTVDNTKFVTSMYNEILILG  316

Qy    354  ARLFPDSNLEAVLNNDGLSPLMWAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP  413
               ||||||||| :||:| | || |:||:|| ||| :|:||:: :|:|||||||||||:|||
Db    317  AKLHPTLKLEEITNRKGLTPLALAASSGKIGVLAYILQREIHEPECRHLSRKFTEWAYGP  376

Qy    414  VYSSLYDLSSLDTCGEEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSFY  472
```

```
Db  377 VHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHDMLLVPENLNRLLQDKWDRFVKRIFY 435
        |:||||||.:.||:| :|||::||||||||||||||:  ::.|:: ::.:||::|| ||
Qy  473 INVVSYLCAMVIFTLTAYYQOPLEGTPPYRTTV-DYLRLAGEVITLFTGVLFFFTNIKD 531

Qy  436 FNFFVVCYLMYIFTAAAYRPVEGLPPYKLKNTVGDYFRVTGEILSVSGGVYFFFRGIQ- 494

Qy  532 LFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYLAGIERAYLAVMVFALVLGWMNALY 591
Db  495 YFLQRRPSLKSLFVDSYSEILFFVQSLFMLVVSVVLYPSQRKEYVASMVFSLAMGWTNMLY 554

Qy  592 FTRGLKLTGTYSIMIQKILFLKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTN 651
Db  555 YTRGFQQMGIYAVMIEKMILRDLCRFMFVLVFLFGFSTAVVTLI-------EDGKN 604

Qy  652 CTVP---TYPSCRDS--------ETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILL 699
Db  605 NSLPMESTPHKCRGSACKPGNSYNSLYST-CLELFKFTIGMGDLEFTENYDFKAVFIILL 663

Qy  700 VTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKLQ 736
Db  664 LAYVILTYILLLNMLIALMGETVNKIAQESKNIWKLQ 700
```

RESULT 2

JC7621

capsaicin receptor, VR1 - human

C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7621
R;Cottright, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.
Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A;Title: The tissue distribution and functional characterization of human VR1.
A;Reference number: JC7621; MUID:21139751; PMID:11243859
A;Contents: Dorsal root ganglia
A;Accession: JC7621
A;Molecule type: mRNA
A;Residues: 1-839 <COR>
A;Cross-references: UNIPROT:Q9H304; GB:AF196175
C;Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a
its integrative activation by several noxious stimuli, and plays an important role in in
C;Genetics:
A;Gene: vr1
A;Map position: 17p13
A;Keywords: transmembrane protein
F;201-233/Domain: ankyrin #status predicted <ANK1>
F;248-280/Domain: ankyrin #status predicted <ANK2>
F;333-365/Domain: ankyrin #status predicted <ANK3>
F;433-455/Domain: transmembrane #status predicted <TM1>
F;477-495/Domain: transmembrane #status predicted <TM2>
F;508-531/Domain: transmembrane #status predicted <TM3>
F;543-569/Domain: transmembrane #status predicted <TM4>
F;578-597/Domain: transmembrane #status predicted <TM5>
F;624-644/Region: pore loop #status predicted
F;656-684/Domain: transmembrane #status predicted <TM6>

Query Match     40.2%;  Score 1551.5;  DB 2;  Length 839;
Best Local Similarity 44.4%;  Pred. No. 1.1e-101;
Matches 320;  Conservative 138;  Mismatches 189;  Indels 74;  Gaps 12;

```
Qy   49 PSPADASRPAGPGDGRPNL------RMKFQG-----AFRKGVPNPIDLLES--TLYESSV 95
        :|:||:.:   : :  :| ||||||   ::  |::  ||
Db    1 PDPLDGDPNSRPPAKPQLSTAKSRTRLFGKGDSEEAFPVDCPHEEGELDSCPTITVSPV 81

Qy   96 V-------PGPKKAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVF 149
        |                 :::       ||:|:
Db   82 ITIQRPGDGPTGARL----------------LSQDSVAASTEKTLRLY 113

Qy  150 NRPILFDIVSRGSTADLDGLLPFLITHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDT 209
        | |:|: :: :|:| |||   | |:  :::::| || .:|| :: ::::|.|.||||:
Db  114 DRRSIPEAVAQNNCQDLESLLLFLQKSKGHLTDNEFKDPETGKTCLLKAMLNLHDGQNTT 173

Qy  210 IPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQAR 269
        ||| :||:| |:|||||:|||:|||||||||||||||: ||||||||||||||||:|:|||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQAR 269
```

RESULT 3

JC7796

epithelial calcium channel 2, ECaC2 - mouse

N;Alternate names: calcium T1; CaT1
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-2002 #sequence_revision 17-May-2002 #text_change 09-Jul-2004
C;Accession: JC7796
R;Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A;Title: Gene structure and regulation of the murine epithelial calcium channels ECaC1 ar
A;Reference number: JC7796
A;Accession: JC7796
A;Molecule type: DNA
A;Residues: 1-727 <WEB>
A;Cross-references: UNIPROT:Q91WD2; GB:AF336378
C;Comment: This calcium channel plays an important role in active transcellular calcium a
relevant for in vivo calcium homeostasis.
C;Genetics:
A;Gene: ECaC2
A;Map position: 6
A;Introns: 43/2; 76/1; 117/1; 163/1; 196/1; 253/3; 302/3; 373/3; 402/3; 428/2; 483/3; 50€
C;Keywords: calcium channel

Query Match     19.1%;  Score 736.5;  DB 2;  Length 727;
Best Local Similarity 33.3%;  Pred. No. 4.4e-44;
Matches 196;  Conservative 101;  Mismatches 193;  Indels 99;  Gaps 21;

```
Qy  183 EEFREPSTGKTCLPKALL--NLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
        : .:||||||||| ||     :::||:|| ||
Db   71 EVHQRGAMGETALHIAALYDNL------EAAMVLMEAAP-----ELVFEPMTSELYEGVT 119

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300
        |||:|:|||:|||||||||||||||:|:|  |:  || || :| |||.|   :||:|||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQAR 300
```

```
Db  174 IPLLLEIARQTDSLKELVNASYTDSYYKGQTALHIAIERRNMALVTLLVENGADVQAAAH 233
        |:||| : .: :||||||::||. ||  ||||||||||: : :|||||||||||| ||||
Qy  270 GRFFQPKDEGGYYFGELPLSLAACTNQPHIVNYLTENPKKADMRRQDSRGNTVLHALV 329

Db  234 GDFFKKTKGRPGPFYFGELPLSLAACTNQGIVKFLLQNSWQTADISARDSVGNTVLHALV 293
        ||::|   ||||| |||||||||||||||  |||||||||  |   .|.|.||||||||||
Qy  330 AIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHI 389

Db  294 EVADNTADNTKFVTSMYNEILMLGAKLHPTLKEELTNKKGMTPLALAAGTGKIGVLAYI 353
        |.|:||:|.||||.||:.|| || |||.  |:|||| :||||| || |: ||||: | |
Qy  390 IRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTGEEASVLEILVY-NSKIENRHE 448

Db  354 LQREIQEPECRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412
        ||:||:|||||||||||  ||||||:|||||||  |||  |||||||||||||||||||||
Qy  449 MLAVEPINELLRDKWRKPGAVSPYINVVSYLCAMVIFFLTAYYQOPLEGTPPYRTTVDY 508

Db  413 MLLVEPLNRLLQDKWDRFVKRIFYFNFVVCYLMYIFTAAAYRPVDGLPPFKMEKIGDY 472
        |||||| ||||||||    |||::  |.|| ||:|||.|.||: |.|||:|.|| | ||
Qy  509 LRLAGEVITLFTGVLFPFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAALYL 568

Db  473 FRVTGEILSVLGGVYFFRGIQ-YFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVLYF 531
        |||||||||| ||||||||| |  ||:|||.|||||:||:|:||| ||||||  |||||
Qy  569 AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFLKDLFRPLLVVLLFMIGY 628

Db  532 SHLKEYVASMVFSLALGWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVIVFLFGF 591
        :|||||||||||| | ||||||||||| .||| ||||||:||||||||||  :|:|||
Qy  629 ASALVSLLNPCANMKVCNEDQTNCTVPTY------PSCRDSET-----FSTFLLDLFK 675

Db  592 STAVVTLI---------EDGKNDSLPSESTSHRWRGPACRPPDSSYNSLYST-CLELFK 640
        |:||||:|           ::|:||  : :. :.|| .| | .|| :||||| ||||||
Qy  676 LTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKL 735

Db  641 FTIGMGDLEFTENYDFKAVFIILLLAYVILTYILLLNMLIALMGETVNKIAQESKNIWKL 700

Qy  736 Q 736
        |
Db  701 Q 701
```

```
Db  120 ALHIAVINQVNVNLVRALLARGASVSARATGSVFHYRPH-NLIYYGEHPLSFAACVGSEEI 178
            ||:||:|||            |||:||:: :  :|||||||:  :||:|:||::|:
Qy  208 NKTFACQMYNLLSLYDRHGDHLQPLDLVPNHQGLTPFKLAGVEGNTVMFQHLMQK----- 262

Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFV------------LKC 353
            |::|          ||:||||||||||||  ||
Qy  398 DTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVVNSKIENREHLAVEPINE 457

Db  179 VRLLIEH--GADIRAQDSLGNTVLHILV-------LQPNKTFACQMYNLLSLYDGGDHLK- 229
            |:: |  ||||||||||||||:|::|      ::|
Qy  263 ----RKHTQWTYGPLTSTLYDLTEIDSSGDEQSLLELIITTKKREAR-QILDQTPVKE 315

Qy  354 ARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGP 413
            :|:|||            ||::|:|::|||     ||:||||  |
Db  230 ------SLELVPNNQGLTPFKLAGVEGNTIVMFQHLMQK--------RKHIQWTYGP 271

Db  414 VYSSLYDLSSLDTCGEEASVLEILVVNSKIENREHLAVEPINELLRDKWRKFKGAVSFYI 473
            :|||||||:       ||:||::: :|||          ||||||||||||||
Qy  501 PYRTTVDYLRLAGEVITLFTGVLFFFNIKDLFMKKCPGVNSLF-----IDGSFOLLYFIY 556

Qy  474 NVVSYLCAMVIFTLTAYYQPLE------GTPP------YPYRTTVDYLRLAGEVI 516
            ::::|||||:||| |            |||           ||:||||:|||||
Db  272 LTSTLYDLTEIDSSGDDQSLLELIVTTKKREAR-QILDQTPVKELVSLKWKRYGRPYFCV 330

Db  331 LGAIVLYLIICFTMCCVYRPLKPRITNRTNPRDNTLMQQKLLQEAVVTPKDDLRLVGELV 390
            |::|:|||:::||                :::|:    ||:||||||||||
Qy  557 SVLIVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFR 616

Qy  517 TLFTGVLFFFNIKDLFMKKCPGVNSLF------IDGSFOLLYFIYSYVLIVVSAALYLAGIE 572
            ::::| |::: ::|:                 :|| |
Db  391 SIVGAVIILLVEIPDIFRL--GVTRFFGQTILGGPFHVIIITYAFMLVTMVMRLTNVD 447

Db  573 AYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFPLLVYLLFMIGYASAL 632
            |:|||::|||:|||:|:::|||:             |  ::|   ||::|::|::|:
Qy  617 FLLIVYLLFMIGYASALVSLLNPCANMKVCNEDQTNC-TVPTYPSCRDSETFSTFLLDLFK 675

Qy  573 AYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFPLLVYLLFMIGYASAL 632
            :||||| |:::|::| ||:::|:|::|:             |    ||::|:::||:
Db  448 GEVVPMSFALVLGWCNVMYFARGFQMLGPFTMIQKMIFGDLMRFCWLMAVVILGFASAF 507

Db  633 VSLLNPCANMKVCNEDQTNC-TVPTYPSCRDSETFSTFLLDLFKLTIGMG----DLEMLS 687
            |||     ||::::|         ||:::|:  ||||||||||::|:|
Qy  676 LTIGMGDLEMLSSTKYPVVFIILLVTYYILTFVLLLNMLIALMGETVGQVSKESKHIWKL 735

Qy  508 YIIFQ-------------TEDPDELGHFYDYPMA----||:|:|-|LFSTF--ELF-LTIIDGPANYDVDL-- 550
            ||:|             ||:::|:|||||             ||||:  ||| |||:||||
Db  493 FCWLMAVVILGFASAFYIIFQ------------------TEDPEELGHFYDYPMA-----LFSTF--ELF- 537

Qy  688 STKYPVVFIILLVTYYILTFVLLLNMLIALMGETVGQVSKESKHIWKLRAQ 736
            :|:|||||||||||||||||||||:::|:::|||||:|::||||||||
Db  538 LTIIDGPANY--NVDLPFMYSTTYAAFAIIATLLMLNLLIAMMGDTHWRVAHERDELWRA 595

Qy  551 ---PFMYSVTYAAFAIIATLLMLNLLIAMMGDTHWRVAHERDELWRAQ 595

Qy  736 Q 736
Db  596 Q 596
```

RESULT 4
JC7531
calcium transport protein, CaT1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev, P.M.; Brown
Biochem. Biophys. Res. Commun. 278, 326-332, 2000
A;Title: Human calcium transport protein CaT1.
A;Reference number: JC7531; MUID:20551480; PMID:11097838
A;Molecule type: mRNA
A;Residues: 1-725 <PEN>
A;Cross-references: UNIPROT:Q9H296; GB:AF304463
C;Comment: This protein, a member of a family of Ca2+ channels, has a role in cellular c
ine and kidney.
C;Genetics:
A;Gene: CaT1
A;Map position: 7q33-34
C;Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane protein

Query Match      18.8%;  Score 724.5;  DB 2;  Length 725;
Best Local Similarity 32.9%;  Pred. No. 3.1e-43;
Matches 198;  Conservative 98;  Mismatches 218;  Indels 87;  Gaps 20;

```
Qy  171 PFLLTHK-------KRLTDEBFR--EPSTGKTCLPKALL--NLSNGRNDTIPVLLDIA 217
            ||:|:       |::||:|   |::|::|||| |    |:|:|||||:||:||::|
Db   48 PLLLAAKDNDVQALNKLLKYEDCKVHRGAMGETALHIAALYDNL------EAAMVLMEAA 102

Db  218 ERTGNMREFINSPFRDIYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKD 277
            ::|||||||||||||||||||:|||||:|||||| |||||||||:|:|| |||::|
Qy  103 P------ELVFEPMTSELYEGQTALHIAVVNQMNLVRALLARRASVSARATGTAFR-RS 155

Qy  278 EGGYFYPGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRE 337
            ||||:||||||||||| ||||| |:||||||||||||||||||||:|||||:||||||
Db  156 PCNLIYFGEHPLSFAACVNSEEIVRLLIEH-----GADIRAQDSLGNTVLHILI----LQP 207

Qy  338 NTKFVTKMYDLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDE 397
```

RESULT 5
JC7795
epithelial calcium channel 1, ECaC1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
R;Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A;Title: Gene structure and regulation of the murine epithelial calcium channels ECaC1 an
A;Reference number: JC7795
A;Accession: JC7795
A;Molecule type: DNA
A;Residues: 1-723 <WEB>
A;Cross-references: GB:AF336378
C;Comment: This calcium channel plays an important role in active transcellular calcium a
relevant for in vivo calcium homeostasis.
C;Genetics:
A;Gene: ECaC1
A;Map position: 6
A;Introns: 37/2; 70/1; 111/1; 157/1; 190/1; 247/3; 296/3; 367/3; 396/3; 422/2; 477/3; 500
C;Keywords: calcium channel

Query Match       18.6%;   Score 719;   DB 2;   Length 723;
Best Local Similarity 33.3%;   Pred. No. 7.6e-43;
Matches 201;   Conservative 100;   Mismatches 198;   Indels 104;   Gaps 23;

```
Qy  173 LLTHKKRLTDE-EFRE-PSTGKTCLPKALL-NLSNGRNDTIPVLLD----IAERTGN 222
            |::||:|:| |:|   |::|:||||  |:||:|||||:||:||      :
Db   52 MCTLKKLQHDQNCDFRQRGALGETALHVAALYDNL------DAAIMEAAPYLVTEST- 104

Db  223 MREFINSPFRDIYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYF 282
            |||:| |:|||||||:|||||:|||||| |||||||||:|::|| |||::||:
Qy  105 ----LCEPF----VGQTALHIAVMNQVNLVRALLARGASASARATGSAFH-RSSHNLI 154

Qy  283 YFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFV 342
            |:|| |||||| ||||| |:|||||||||||:|||||||||:||||||::|||||
Db  155 YYGEHPLSFAACVGSEEIVRLLIEH--GADIRAQDSLGNTVLHILV----LQPNKTFA 206

Qy  343 TKMYDLLL----LKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVT 395
            ||:||||        :||:|||:|||||||:|||||||||||||||||||||||
Db  207 CQMNLLSLYDGGDHLK------SLELVPNNQGLTPFKLAGVEGNTVMFQHLMQK--- 255
```

Qy 510 RLAGEVITLFTGVLF------------------------FFTNIKDLFMKKCPGVNSLFIDGSFQLLY 553
         :::||:                                  ::|.|:
Db 431 RTACELLTILNCIFFVGYQQLGEIRTQMRGYLRNLKTAPAKAVFCIANLFL------ 482

Qy 554 FIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGYSIMIQKILFKD 613
         :.|          :::::::||
Db 483 ---LLCIPPRLMKKHEIEE--ALFVFALPGSWIFLLFFARSAKLTGPFVQMIYSMIAGD 536

Qy 614 LFRFLLVLLFMIGYASALVSL-LNPCANMKVCNEDQTNC----TVPTYPSCRDSETFS 667
        :.::  .| .: :       :: :                    .::::PSCRDSETFS
Db 537 MIRFAIISAIFLVSFSQVFYFVGKDMDAKQKLEDTNPHACRISGYTIYTY-----NTFP 590

Qy 668 TFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSK 727
          : :|   .:||   :|.:.::.||::|:|::.||:.|:.|::|.|::||:||.|
Db 591 ETFITLFRASMGDYDYEFSCANYQALTKTLFVLYMFVMPIMMINILIAMGNTYTTVIA 650

Qy 728 ESKHIWKLQ 736
         .: :|
Db 651 QAEKAWRQQ 659

RESULT 7
D88651

protein B0212.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D88651
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans; a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: D88651
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-957 <STO>
A;Cross-references: UNIPROT:O17469; GB:chr_IV; PIDN:AAC02569.1; PID:g2854148; GSPDB:GN00(
A;Note: contains similarity to ankyrin repeats
C;Genetics:
A;Gene: B0212.5
A;Map position: 4

Query Match        12.3%;      Score 473.5;     DB 2;    Length 957;
Best Local Similarity    27.1%;     Pred. No. 2.7e-25;
Matches 149;    Conservative   90;    Mismatches 213;    Indels   97;    Gaps   17;

Qy 233 DIYYR---GQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPK----------DEG 279
        ||::|   |.:||:|||| :  : :|||:.:.|||.|||.||.||
Db 166 DIYLGDEQFGQSALHLAIVHDDYETVSLLLNSKADVNARACGNFFLPEDFKLTNKITDYQ 225

Qy 280 GYFYFGELPLSLAACTNQPHIVNYLTE---NPHKKADMRRQDSRGNTVLHALVAIADNTR 336
        ||.|:||.||:.|||.  :.|  .| .   ||         |::GNT:LH.:V
Db 226 GYAYYGEYPLAFAACFGNKDIYDLLIQFGANPN------LQDSFGNTILHMCV-------- 272

Qy 337 ENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIRREVTD 396
         |             ::  :::  :::||..:.|: |::.|.: |:: :|:..::
Db 273 --INYSSSMYSYAVRHWAK--PAD--PHVVNHAGFTPLTLATKLGRKQIFEEMLE------ 321

Qy 397 EDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASV---LEILVVNSKIENRHEMLAV 452
           .    :   : |      .:.:|.:  :|:..:..   :.::|:|: ||.|.:::.
Db 322 --IMKVEFWRFSDMTCSAYPLNTLDTIQPDGSTNYDSALMTVINGSTPEHLDMIGS 375

Qy 453 EPINELLRDKWNRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPYPYRTTV---DYL 509
        | |::||.|||...||...:.|..:.||.|::|| |:.:| ||.    :  |   ||
Db 376 EVIQRLLADKWKAFAQRKLIERLVLLIVQLITLSIVVYIRPTE--LPRLYMEDPQWDDYI 433

Qy 510 RLAGEVITLFTGVLF------------------------FFTNIKDLFMKKCPGVNSLFIDGSFQLLY 553
         :::||:                                  ::|.|:
Db 434 RTACELLTILNCIFFVGYQQLGEIRTQMRGYLRNLKTAPAKAVFCIANLFL------ 485

Qy 554 FIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGYSIMIQKILFKD 613

---

Qy 396 DEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVVNSKIENRHEMLAVEPI 455
          ::     ::   :.|      .:.:|.:  :|:..: ::.::|:|: |:.|.:::.
Db 256 ------RKRIQWSFGPLTSSLYDLTEIDSNGEELSFLELVVSSKKKEAR-QILEQTPV 306

Qy 456 NELLLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPL----------EGTP 498
         |::|.||....||..:.|..:.||.|::|| |:.:| ||          |.||
Db 307 KELVSLKWKKYGQPYFCLLGALYIFYMVCFTTCCVVRPLKFRDANRTHVRDNTIMEQKSL 366

Qy 499 PYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLF----IDGSFQLLYF 554
        |   |   ||  :::||:                :::.|:         :|:.|.
Db 367 QEAYVTYQDKIRLVGELVTVIGAVIILLEIPDIFR--VGASRYFGQTVLGGPFHVIII 423

Qy 555 IYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGYSIMIQKILFKDL 614
        .|          :::::::||           |.  :|:||:.:.|..:.|||.:| |:|
Db 424 TYASLVLLTMAMRLTNVNGEVVPMSALVLGWCSVMYFARGFQMLGPFTIMQKMIFGDL 483

Qy 615 FRFLLVLLFMIGYASALVSLLNPCANMKVCNEDQTNC-TVPTYPSCRDSETFSTFLLDL 673
        .:::  .| .: :       :: :              .::|:PSCRDSETFSTF: :|
Db 484 LRFCWLMAMVLGFASAFYIIFQ-------TEDPDNLGEFSDYPTA---MFSTF--EL 529

Qy 674 FKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIW 733
        |.|  .:||   :|.:.::.||::|:|::.||:.|:.|::|.|::||.|.|: .: :|
Db 530 F-LTIIDGPANY--RVDLPFMYSVTYATFAIIATLLMLNLFIAMMGDTHWRVAQERDELW 586

Qy 734 KLQ 736
        :|
Db 587 RAQ 589

RESULT 6
T37241

olfactory channel protein osm-9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37241
R;Colbert, H.A.; Smith, T.L.; Bargmann, C.I.
J. Neurosci. 17, 8259-8269, 1997
A;Title: OSM-9, A novel protein with structural similarity to channels, is required for
A;Reference number: Z21639; MUID:97477445; PMID:9334401
A;Accession: T37241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-937 <COL>
A;Cross-references: UNIPROT:O17469; EMBL:AF031408; NID:g2642589; PIDN:AAB87064.1; PID:g2
C;Genetics:
A;Gene: osm-9
A;Map position: IV
C;Keywords: transmembrane protein

Query Match        12.3%;      Score 473.5;     DB 2;    Length 937;
Best Local Similarity    27.1%;     Pred. No. 2.6e-25;
Matches 149;    Conservative   90;    Mismatches 213;    Indels   97;    Gaps   17;

Qy 233 DIYYR---GQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPK----------DEG 279
        ||::|   |.:||:|||| :  : :|||:.:.|||.|||.||.||
Db 163 DIYLGDEQFGQSALHLAIVHDDYETVSLLLNSKADVNARACGNFFLPEDFKLTNKITDYQ 222

Qy 280 GYFYFGELPLSLAACTNQPHIVNYLTE---NPHKKADMRRQDSRGNTVLHALVAIADNTR 336
        ||.|:||.||:.|||.  :.|  .| .   ||         |::GNT:LH.:V
Db 223 GYAYYGEYPLAFAACFGNKDIYDLLIQFGANPN------LQDSFGNTILHMCV-------- 269

Qy 337 ENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIRREVTD 396
         |             ::  :::  :::||..:.|: |::.|.: |:: :|:..::
Db 270 --INYSSSMYSYAVRHWAK--PAD--PHVVNHAGFTPLTLATKLGRKQIFEEMLE------ 318

Qy 397 EDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASV---LEILVVNSKIENRHEMLAV 452
           .    :   : |      .:.:|.:  :|:..:..   :.::|:|: ||.|.:::.
Db 319 --IMKVEFWRFSDMTCSAYPLNTLDTIQPDGSTNYDSALMTVINGSTPEHLDMIGS 375

Qy 453 EPINELLRDKWNRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTV---DYL 509
        | |::||.|||...||...:.|..:.||.|::|| |:.:| ||.    :  |   ||
Db 376 EVIQRLLADKWKAFAQRKLIERLVLLIVQLITLSIVVYIRPTE--LPRLYMEDPQWDDYI 430

```
Qy    576  -AVMVPALVLGWMNALYFTRGKLKTGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALV  633
                 :: :||: ::|: :  ||:|:  ||:| : :|:||:::|| ||||:|| : ::
Db    589  DNVLITVTMIFTTVHYLYYCRVIRFVGPFVLMVYTIIATDIFRRMLIYGIFLMGFSQSFS  648

Qy    634  SLLNPC---AN-MKVCNEDQTNCT-------------VPTYPSC--RDSETFS-------  667
                  |:| :  :|:|  |:             ::     :
Db    649  LIFLSCREEANVIKKLITDQSEASEGSDNKFNLTRQISAYDTAIVKNAEVFENVMQSPIE  708

Qy    668  ----TFLLDLFKLTIGMGDLEMLSSTKYPVVPFIILLVTYIILTFVLLLNMLIALMG---E  720
               ||:|| ||:|||::  ::        |::| ::|| ||| :|::||:|:
Db    709  AFVRTFILTIGEPTVLYRNLALCPANTMWIGKVVFILFELFVSIMQFNMLIAMMTRTYE  768

Qy    721  TVGQVSKESK  730
           |:|:||::|
Db    769  TIFQTQLEYK  778
```

```
RESULT 9
T20312
hypothetical protein F28H7.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20312; T21533
R;Matthews, P.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19255
A;Accession: T20312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-790 <WIL>
A;Cross-references: UNIPROT:P90784; EMBL:Z74030; PIDN:CAA98449.1; GSPDB:GN00023; CESP:F28H7.10
A;Experimental source: clone D1054
R;Berks, M.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19435
A;Accession: T21533
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-790 <WI2>
A;Cross-references: EMBL:Z72508; PIDN:CAA96644.1; GSPDB:GN00023; CESP:F28H7.10
A;Experimental source: clone F28H7
C;Genetics:
A;Gene: CESP:F28H7.10
A;Map position: 5
A;Introns: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 67§

Query Match          8.1%;  Score 313.5;  DB 2;  Length 790;
Best Local Similarity   22.0%;  Pred. No. 4.4e-14;
Matches  155;  Conservative  94;  Mismatches 209;  Indels 245;  Gaps  28;
```

```
Qy    152  PILFDIVSRGSTADLDGLLPFLLTHKKRL-------------TDEEFRE------PSTGK  192
                ::|  :| ||:|:|::|| ||:||::|         ||    :::
Db    109  PNILDEFDQGQ-AEMAGDL----------KKALKLLDGGKGKSESKYREMVWSVDERGSMGE  161

Qy    193  TCLPKALLNLSNGRNDTIPVLLDIAERTGN-MREFINSPFRDIYRGQTALHIAIERRCK  251
                ||||:|  ::| || |::                  :: ||
Db    162  NLLAICLLQGSALHN------LIARRLINFFPPLINDICVSEEYYGLSPLHLAIVNQDA  214

Qy    252  HYVELLVAQGADVHAQARGRFFQPKDE-------------GGYFYFGELPLS  290
              ||:  ::| ||::           ::|:
Db    215  QFTSLLLRLGADLNQRCYGAFFCADDQKASRTDSLEHEFVELTKNTNYTGSMYFGEYPLS  274

Qy    291  LAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTMYDLLL  350
              |   |: |   ||:|      ||:| ::||:|:|  ||: ||:|:|:|: ::
Db    275  FAICMGQHDLFRMLLA--KKANLSAQDTNGNTALH-LCVIHD--------KM-DML-  318

Qy    351  LKCARLFPDSNLEA--------VLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRK  405
              |||:||::| :        ||| :| | :::  | |:| :|  |::|::
Db    319  --DAVLEAGGNIRLANKQNLTALTLAARLAK------------KTESIQHLE--  356

Qy    406  FKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVVNSKIENRHEMLAVEPINELLRDKWRK  465
              ::||:    :|:: ::  :: :|  |:| :::| :::::  :||::|: ::
Db    357  ----------------------------------------LMDGLIEQILDEKWKA  372
```

```
RESULT 8
T33026
hypothetical protein T09A12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33026
R;Hawkins, J.; Fulton, B.; Gillam, B.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid T09A12.
A;Reference number: Z21265
A;Accession: T33026
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-900 <HAW>
A;Cross-references: UNIPROT:O61220; EMBL:AF047660; PIDN:AAC04431.1; GSPDB:GN00022; CESP:
A;Experimental source: strain Bristol N2; clone T09A12
C;Genetics:
A;Gene: CESP:T09A12.3
A;Map position: 4
A;Introns: 43/2; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 780/3; 82

Query Match          11.3%;  Score 435.5;  DB 2;  Length 900;
Best Local Similarity   24.9%;  Pred. No. 1.2e-22;
Matches  167;  Conservative  99;  Mismatches 231;  Indels 173;  Gaps  26;
```

```
Qy    189  STGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIY----YRGQTALHI  244
              |:| ||||:| ::| || |::                      :| ||
Db    154  SMGETIIGCCLLHASDIHNALVLKILDYYPKLLN-----------DIHISEDFYGLSPLHQ  203

Qy    245  A-IERRCKHYVELLVAQGADVHAQARGRFFQPKDE----------GGYF  282
            | |: || :| ::|  ::|  :                   ::|
Db    204  AIINTDCK-LVYKFLKLGADVNSRCYGAFFCADDQKASRTDSLEHEYEVELSLKTNYTGNM  262

Qy    283  YFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFV  342
            |||: ||:|   ||| |   ||:|      ||:| ::| |:|  ||: ||:|:|:|:
Db    263  YLGEYPLSFAACLNQPESFRLLA---FKANPNAQDTNGNSVLHMCV-----IHENMAMF  314

Qy    343  TKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHL  402
                  ||:|:||:||| | :    |:||| |||:::     :| |:| :|: :|::||
Db    315  K-----LALECG--ASLRTV-NKQSLSPLTLAAKLAKKEMPDEILELEGDSV-----  358

Qy    403  SRKFKDWAYGPVYSSLYDLSSLDTCGE-------EASVLEILVYNSKIENRHEMLAVEPIN  456
               |||:||:     :|:: ::   ::          ::|  :||::::::  :||::|
Db    359  --WAYGDASSTAYPLAKIDTINETTGELNEASALSLVVYGQTVE--HLELLDGLLD  410

Qy    457  ELLRDKWRKFG---AVSFYINVVSYLCAMVIFTL-------------TAYYQPLEG-  496
               ::||:|:|     | |:|::|| |||:|                :|::|
Db    411  TLLEAKWEAFAKRNMIVSFTAFTLYYICFVTAFTLRPIGFSTEMLTEGWINRYSEPFGR  470

Qy    497  ---------------------------TPPYPYRTTVDYLRLAGE---VI  516
                                        | :|  ||::|:|::|    |
Db    471  YGKNSTLQQVKPVINATSRGLVEWSEPLSQCHLRNYWDPDIFANS--YIRLVFELFVVI  528

Qy    517  TLFTGVLFFFTNIKDLFMKKCPGVNSLP-IDGSFQLLYFIYSVLIVSAALYLAGIEAYL  575
              ||| ||:|   ::| |:|| | ::|| | |:::|: |:|:|:|::|| |:| |::||:
Db    529  GICVQVFLDFRDIKRIGRKKWWNVLTAFPAKITFKLIYFLVLAMIPTRLACDLSPVLLVV  588

Qy    486  ----LLCIPFRLMKKHEIEE--ALFVPALPGSWIFLLFFARSAKLTGPFVQMIYSMIAGD  539
              ::: |   :|:  |||| ::    |:|:   :| ::|     |: ||   ::
Db    614  LFRFLLVYLLFMIGYASALVSL-LNPCANMKVCNEDQTNC------TVPTYPSCRDSETFS  667

Qy    540  MIRFAIISAIFLVSFSQVFYFVGKDMDAKQKLEDTNPHACRISGYTIYTY-------NTFP  593
              |:|::  :|:|:|:   || : |: :  |        | :  || :|     |||
Db    668  TFLLDLFKLTIGMGDLEMLSSTKYPVVPFIILLVTYIILTFVLLLNMLIALMGETVGQVSK  727

Qy    594  ETFITLFRASMGGYDYEEFSCANYQALTKTLFVLYMFVMPIMMINILIAMGNTYTTVIA  653
               ||| |::    ||       |: ::||| ::| ||:  ::  ::::||| :|:|::|
Db    728  ETFITLFRASMGGYDYEEFSCANYQALTKTLFVLYMFVMPIMMINILIAMGNTYTTVIA  653

Qy    728  ESKHIWKLQ  736
             :: |||::|
Db    654  QAEKAWRQQ  662
```

Qy 466 FGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTVD----------- 507
Db 373 YGRALWLRSLLGFIFFYCCFVCAYMLRPSSAATEHLTRGRINDDGETESTNSTNYLQWHA 432

Qy 508 ----------------YLRLAGEVITLFT--GVLFFFTNIKDL------FMKKCPG 539
Db 433 IDTQCHLMYYSAWPWTHGWFRLGCEIMTIIVMLFQILLDFGDIRRIGFQKWFNFLKAFPA 492

Qy 540 VNSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAV-----MVFALVLGWMNALYFTRG 595
Db 493 --KLMFKGAF--LFIIISIPCRLACSFH----EFFLTIDNTMAIISILLVTQHFLYYMRA 544

Qy 596 LKLTGTYSIMIQKILFKDLFRFLLVLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVP 655
Db 545 IPFVGPFVLMVYTIIATDLVRFAMIYSIFLVGFSQSFYLIFTSCE----------- 589

Qy 656 TYPSCRDSETF-------STF------LLDLFKLTIGMGDL---EMLSSTKYPVVF 695
Db 590 -----RDSTAIKKIDEMGSEFNNIMENPVDALLRTFIMTIGEFSVLYREMSACDNFWMKW 644

Qy 696 IILLVTYIILTFVLLL--NMLIALMG--ETVGQVSKESKHIW 733
Db 645 IGKLIFVIFETFVSIIQFNLLIAMMRTYETIFLTRKEWKRQW 687

RESULT 10
T24772
hypothetical protein T10B10.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24772
R;Sims, M.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19934
A;Accession: T24772
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-519 <WIL>
A;Cross-references: UNIPROT:Q22374; EMBL:Z72514; PIDN:CAA96679.1; GSPDB:GN00028; CESP:T10B10
C;Genetics:
A;Gene: CESP:T10B10.7
A;Map position: X
A;Introns: 47/3; 139/1; 183/1; 215/2; 249/1; 385/3; 440/3

Query Match    7.2%;  Score 278;  DB 2;  Length 519;
Best Local Similarity 29.5%;  Pred. No. 7.9e-12;
Matches  89;  Conservative  36;  Mismatches 115;  Indels  62;  Gaps  10;

Qy 216 IAERTGNMREFINSPF-RDIYR--GQTALHIAIERRCKHYVELLVAQGADVHAQARGRF 272
Db 161 VKQMYRFPKIVNDIFLSEEYYASVGLSPLHQAIVNEDLEMVYFLCRKGADVHQRCYGSF 220

Qy 273 FQPKDE-------------GGYFYGELPLSLAACTNQPHIVNYLTENPHKK 311
Db 221 FCADDQKASRTDSLEHEWDLVQSTKYTGQMYWGEYPLSFAACTNQVDCFRLLRA--MK 277

Qy 312 ADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGL 371
Db 278 ADPNMPDTNGNTVLH-----------LTVIHDLPEMFMLAVELGANLH-VRNNLKL 321

Qy 372 SPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEE- 430
Db 322 TPLALAARLAKKHIYDLILE---CDMDI-------SWRYGPVVCKAYPLNDVDTINESD 370

Qy 431 ----ASVLEILVVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIF 485
Db 371 GSLNPNSVIANVVYGDKVD--HLEFFPDGLIEEVLESKWETFGKKQLFMSLAGYIYFLAVF 428

Qy 486 TL 487
Db 429 YL 430

RESULT 11
T19552
hypothetical protein C29E6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19552
R;Dobson, R.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19141
A;Accession: T19552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1188 <WIL>
A;Cross-references: UNIPROT:Q18297; EMBL:Z72504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C2!
C;Genetics:
A;Gene: CESP:C29E6.2
A;Map position: 4
A;Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

Query Match    5.3%;  Score 204.5;  DB 2;  Length 1188;
Best Local Similarity 20.3%;  Pred. No. 4.1e-06;
Matches 152;  Conservative  98;  Mismatches 250;  Indels 247;  Gaps  33;

Qy 124 RKKIIEKQPQSKAPAPQPPPILKVFNRPILFDIVSRGSTADLD---------GLLPFLLT 175
Db 418 RKKNKETERSALKSPTRNTLRIVSEDVRRTMVNMVDRDQNTPMHIVASNGYLEMMQLLQK 477

Qy 176 HKKRLT---DEFFRBPSTGKTCLPKALLNL-------------------SNG 205
Db 478 HGASITQVNEDE---------------TALHRAAIGVRQLLEWDIRLLLMKDEMGNSALHLAARSG 529

Qy 206 RNDTIPVLLDIAERTGNMREFINSPFRDIYRGQTALHIAIERRCKHYVELLVAQGADVH 265
Db 530 HDATTKVLLD----------NGADKEAKNS------YQ-KTPLQVAVDSGKLETCQRLVAKGAQIE 578

Qy 266 AQ--------------------ARGRFFQPKDEGGYFYGELPLSLAACTNQPHIVN 302
Db 579 SSSDTKTVLHTAAFYGNESIVRYFIAEGVTIDRRDEEGKTAFD-------IAC------- 624

Qy 303 YLTENPHKKADMRR------QDSRGNTVLHALVAIAD-----NTRENTKF---VTKMYDLL 349
Db 625 --ENDHK--DVARAFLETDQWKNLMIPCDVIPLDKHRNPVNMKRRTPFRTLLTKFFBLA 679

Qy 350 ----------LLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIR-REVTDEDTRHL 402
Db 680 SFVMDNCIEKSKEETDSTQSVAVNFEFIDDTYMMRCVSDDGTGEQLIGCKSAYDED----- 735

Qy 403 SRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVVN-------SKIENRHEMLAVEPINE 457
Db 736 ---FKLEKDAQSYASNYD----------------RVYKYTHPLKLMADAEKLH--LLNHPLSK 776

Qy 458 -LLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVI 516
Db 777 ALLKYKWNRLGRPMYYFALFMYL-VFIVSLTQYVRHTKA------PYNVWNEESYYDSE- 828

Qy 517 TLFTGVLFFFTNIKDLFMKKCPGVNSLFID-----------GSFQLLY 553
Db 829 ------YFDEN------ETCPQINTTKPDVVWKIIIQTLAVCQILVECFQLFQRKFAYL 875

Qy 554 --------FIYSVLVIV---SAALYLAGIEAYLAVMVFALVL--GWMNALYFTRGLKL 598
Db 876 VNWENWIDCFIYSTALITVYDFSECSATSGVRQNWQWILAALCIFFGWINLLFMIRKMPR 935

Qy 599 TGTYSIMIQKILFKDLFRFLLVLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYP 658
Db 936 FGIFVVMFVDIV-KTFFRFFPVFVLFIIAFSSSFYVL------------------- 972

Qy 659 SCRDSETFSTFLLDLFKLTIGM-------GD---LEMLSSTKYPVVFILLLVTYI 703
Db 973 -QNRPFSTIFMSPLKTTVMMIGEFEFTGIFHGDETTHAEKMFGPAHTAVACALFFFC 1030

```
Qy    704  ILTFVLLNMLIALMGETVGQVSKESK  730
           |:.||||||:|||||||||||||||
Db   1031  IIMTILLMNLLVGLAVDDIKGVQEKAE 1057
```

Db    664  DVEWK 668
           ||
           DVEWK

RESULT 12

JC5807

trp3 protein - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
C;Accession: JC5807
R;Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I.
Biochem. Biophys. Res. Commun. 240, 167-172, 1997
A;Title: Expression and characterization of a trp1 homolog from rat.
A;Reference number: JC5807; MUID:98042538; PMID:9367904
A;Accession: JC5807
A;Molecule type: mRNA
A;Residues: 1-828 <PRE>
A;Experimental source: brain
C;Comment: This protein participates in store-operated Ca2+ entry into cells.
C;Superfamily: TRPC3 protein

Query Match    4.9%;   Score 188;  DB 2;  Length 828;
Best Local Similarity  20.6%;  Pred. No. 3.6e-05;
Matches  137;  Conservative 100;  Mismatches 240;  Indels 188;  Gaps  31;

Qy    210  IPVLLDDIAERTGNMREFINSPFRDIYRGQTALHIAIERRCKHYVELL------VAQGADV 264
           |||  :.:|||  .|::|  |||||:|  ||||:||:|| ||||||||      ||  ||.
Db     52  IPVVRKMLEESRTLN--VNC---VDYMGQNALQLAVGNEHLEVTELLLKKENLARIGDA  105

Qy    265  ----------------HAQARGRFFQP---KDEGGYFVFGE------LPLSLAA  293
                            |:|| .| ||      |:|||| ||       ||| ||
Db    106  LLLAISKGYVRIVEAILSHPALAQGQTLSPELRDDD--FYYDEDGTRFSPDITPIILAA  163

Qy    294  CTNQPHIVNYL-------TENPH----KKADMRRQD------------SRGNTVLHALVAIADNT  335
           |: | |:.:.        :.||.    |||  ||                  ||::|||:||||:
Db    164  HCHKYEVVHLLLKGRTERPHDYLCRCADCAEKQRLMTFSHSRSRINAYKGASPGYLSLS  223

Qy    336  RENTKFVTKMYDLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIF-------  386
           |.| |:.|:|||||||:|||||||| .||:.:|||||| |||||:||||:
Db    224  SEDPVLTALELSNELAKLA-------NIEKEFKND-YRKLSMQCKDFVGVLDLCRDSEEV  276

Qy    387  QHIIRREVTDEDTRH-------LSR----KFKDWAYGPVYSSLYDLSSLDTCGEEASV-  433
           |::.||||.|:|                :|||| ||||||||||::||||  |||||:
Db    277  EAILNGDLESVEERHGHKASLSRVKLAIKYEVKKFVAPNCCQQQLLTIWYGNLSGREIAIK  336

Qy    434  -LEILVVNSKIENRHEMLAV-------EPINELLRDKWRKFGAVSFYINVVSYLCAMVIF  485
            |||::|||||||||||::|       ||:|||||:|||||| |||:|||||||||::||
Db    337  CLVVLVVALAL----PFLAIGYWIAPCSRLGKILRSPFMKFVAASFII----FLGLLVF  387

Qy    486  TLTAYYQPLEGTPPYPYRTTVDYLRLAGEV-ITLFTGV-LFFFTNIKDLFMKKCPGVNSL  543
           :|||||||||  ||||:||||||:|| ||  :|||||: |||| |||||||||:|||||
Db    388  NASDRF--EGITTLPNITVIDYPKQIFRVKTTQFTWTEMLIMVWVLGMMWSEC---KEL  441

Qy    544  FIDGSFQLLYFIYSLVIVS----AALYLAGIEAYLA  576
           ||||||||||||||||:||    |||||||||: ||
Db    442  WLEGPREYIVQLWNVLDFLSIFIAAFTARFLAFLQATKAQQYVDSHVQESDLEVTLPPEV 501

Qy    577  -------------------VMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLF 615
                              ::||.||:|||:||.||:|||:||||:||:|||:||||||
Db    502  QYFTYARDKWLPSDPQIISEGLYAIAVVLSFSRIAYILPANESFGPLQISLGRTV-KDIF 560

Qy    616  RPLLVVLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSCRDSETFSTFLLDLFK 675
           |||:|.||||| |||.||||||  ||||:   |.|:|| |||||| ::|  ||| |||
Db    561  KPMVLFIMVFLAFMIGMFILYSYLGAKV---DPAFTTV-------EVITLFTGVLFFTNIKDLF 609

Qy    676  LTIGMGDLEMLSST-KYPVVFI----ILLVTYIILTFVLLNMLIALMGETVGQVSKES 729
           ||:|||| ::|.|  ||:|:       :| |||::||||||||||||||||||||||:
Db    610  LS-------EVTSVVLKYDHKFIENIGVYLYGIYNVTMVVLLNMLIAMINSSYQEIEDDS 663

Qy    730  KHIWK 734
```

RESULT 13

JH0588

calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JH0588
R;Phillips, A.M.; Bull, A.; Kelly, L.E.
Neuron 8, 631-642, 1992
A;Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with h
A;Reference number: JH0588; MUID:92232293; PMID:1314616
A;Accession: JH0588
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1124 <PHI>
A;Cross-references: UNIPROT:P48994; GB:M88185; NID:g469057; PID:g158715
A;Experimental source: head
C;Genetics:
A;Gene: trpl
A;Cross-references: FlyBase:FBgn0005614
C;Superfamily: TRPC3 protein
C;Keywords: calmodulin binding; phosphoprotein; transmembrane protein
F;341-362/Domain: transmembrane #status predicted <TM1>
F;374-396/Domain: transmembrane #status predicted <TM2>
F;462-479/Domain: transmembrane #status predicted <TM3>
F;512-533/Domain: transmembrane #status predicted <TM4>
F;549-572/Domain: transmembrane #status predicted <TM5>
F;643-668/Domain: transmembrane #status predicted <TM6>
F;710-727,809-825/Region: calmodulin binding #status predicted
F;722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match    3.8%;   Score 145.5;  DB 2;  Length 1124;
Best Local Similarity  19.3%;  Pred. No. 0.057;
Matches  141;  Conservative 99;  Mismatches 237;  Indels 253;  Gaps  34;

```
Qy    189  STGKTCLEKALLNLSNGRNDTIPVLLD-----IAERTG--NMREFINSPFRDIYYR-  237
           :.|||:|:| |||: .| ::|||||:       ||| |    |||||||||||:||
Db     24  SVGGCCVPLGLPQ------------------PLLLEEKKFLLAVERGDMPNVRRILQKALRHQHININC  74

Qy    238  ---------GQTALHIAERRCKHYVELLVAQGAD----------------VHAQ  267
                    |||||||:|| :|||||:::|
Db     75  MDPLGRRALTLAIDNENLEMVELLVVMGVETKDALLHAINAEFVEAVELLLEHEELIYKE  134

Qy    268  ARGRFFQPKDEGGYFYFGEL-PLSLAACTNQPHIVNYLTEN----------PH------  309
           :||   .| :|  |||||   || ||  ::| | .|:| |:
Db    135  GEPYSWQKVDINTAMFAPDITPLMLAAHKQNFEILRILLDRGAAVPVPHDIRCCGCEECVR 194

Qy    310  --KKADMRRQDSRGN------TVLHALVAIADNTRENTKF--------------VTKM--YDL 348
             :|||||||| |.      |||:|||||||:|::| |:|              ||||  ||:
Db    195  LTAEDSLRHSLSRVNIYRALCSPSLICLTSNDPSSTAFQLSWELRNLALTEQECKSEYMD  254

Qy    349  LLLKCARLFPD-------SNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTR  400
           |||||||||||       :||:|||:.|||||||||:|||:||||||::|||||:||||
Db    255  LRRQCQKFAVDLLDQTRSNELAIILNYD--------PQMSSVEPG-----------DRM 295

Qy    401  HLSRKFKDWAYGP-----VYSSLYDL-------------SSLD--TCGEEASV--LEI  436
           |||||||:| ||      :|||||:|             ||||  ||||||:   |::
Db    296  SLTRLVQAISYKQKKFVAHSNIQQLLSSIWYDGLPGFRRKSIVDKVICIAQVAVLFPLYC  355

Qy    437  LVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLEG  496
           |||||:|||||:|||||:|||||||||||||:|||:|||||||||||||||||||||||
Db    356  LIYMCAPNCRTGQLMRKPP-----------MKFLIHASSYLPFLFLFILLVS---- 395

Qy    497  TPPYPYRTTVDYLRLAG----------EVITLFTGVLFFFTNIKDLF  533
           :|||||:|||||:|||           |||||||||||||||||||:
Db    396  --QRADDFVRIFGTTRMKKELAEQELRQRGQTPSKLELIVVMYVIGFVWEEVQEIF 450

Qy    534  MKKCPGVNSL-----FIDGSFQLLYFIYSVLIVSVNVTMVVLLNMLIAMINSSYQEIEDDS  580
           |||||||||      ||||||||||||||:|||||::||.||||||||||:|| |||||
Db    451  ---AVGMKSYLRNMWNFIDFLRNSLY--VSVMCLRAFAYIQQATEIARDPQMAYIPREKW  505
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Qy    581  ------ALVLGWMNALYFTRGLKLTGTYSI-----MIQKILFK---DLFRFLLVYLLFMI  626
                 :  ||   : :  | :|           |:|  ||         ||::  |||  |
Db    378  ------WPVLSLCYLIAPK-SQFGRIIHTPFMKFIIHGASYFTFLLLNLYSLVYNEDKK  430

Qy    506  HDFDPQLIAEGLFAAANVFSALKLVHLFSINPHLGPLQISLGRMVIDIVKFFIYTLVLF  565
              | |   | |  :  :   |:|  |::          : |         |:  || :
Db    497  TPPYPYRITVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIY  556

Qy    627  GYASALVSLLNPCANMKVCNEDQTNCTVPTYP-----------SCRDSETFSTFLLDLFK  675
            :  ::||  | ::  :                           |||||:||:|||||:|
Db    431  NTMGPALERIDYL-----LILWIIGMI--WSDIKRLWYE--GLED-FLEESRNQLSFVM  479

Qy    566  AFACGLNQLLMYFAAL-----EKSKCYV-LPGGEADWGSHGDSCMKWRRFG----NLFE  614
                  |   | : | |      :  :||    |  | :| : :           ::|:
Db    557  SVLVIVSAALYLAG-----IRAYLAVMV----FALVLGWMNALYFTRGLKL  598

Qy    676  LT-------IGMGDLEMLSSTKYPVVF-IILLVTYIILTFVLLNLMLIALMGETVGQ  724
                     |  || :| :|: |  |  : |:| | ::|||:||||:||||:||:: :
Db    480  NSLYLATFALKVVAHNKFHDFADRKDWDAFHPTIVAEGLFAFANVLSYLRLFMYTTSSI  539

Qy    615  SSQSLFWASFGMWGLDDFELSGIKSYTRFWGLLMFGSYSVINVIVLNLLIAMMSNNSYAM  674
              ||:  :|| : : | | :  |  ||: || | |:|::|::|| :|||:|||::|:|
Db    599  TGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYP  658

Qy    725  VSKESKHIWK  734
            |::|||:|||
Db    540  LGPLQISMGQML-QDFGKFLGMFLLVLFSFTIGLTQLYDKGYTSK---EQKDC-VGIFC  593

Db    659  SCRDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFI-------ILLVTYI  703
                                                          | |
Db    594  EQQSNDTFHSFIGTCFAL-----FWYIFSLAHVAIFVTRFSYGEELQSFVGAVIVGTYN  647

Db    675  IDEHSDTEWK  684

Qy    704  ILTFVLLNMLIALMGETVGQVSKESKHIWK  734
            ::  :||::   :| ::|| |:|||:||||
Db    648  VVVIVLTKLLVAMLHKSFQLIANHEDKEWK  678
```

RESULT 14

I38361

TRPC1 protein - human

C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 04-Sep-1998
C;Accession: I38361
R;Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.
A;Title: TRPC1: a human homolog of a Drosophila store-operated channel.
A;Reference number: I38361; MUID:96003837; PMID:7568191
A;Journal: Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A;Accession: I38361
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-810 <RES>
A;Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
C;Superfamily: TRPC3 protein

```
Query Match             3.6%;  Score 138.5; DB 2; Length 810;
Best Local Similarity  18.1%;  Pred. No. 0.11;
Matches  147;  Conservative 126;  Mismatches 315;  Indels 223;  Gaps  36;
```

RESULT 15

T00894

hypothetical protein F21B7.8 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00894
R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conv eologis, A.; Ecker, J.R.
A;Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
A;Reference number: Z14208
A;submitted to the EMBL Data Library, January 1998
A;Accession: T00894
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-616 <SHI>
A;Cross-references: UNIPROT:Q9LR59; EMBL:AC002560; NID:g2618677; PID:g2809239; GSPDB:GN0(
C;Genetics:
A;Gene: ATSP:F21B7.8
A;Map position: 1
A;Introns: 229/1; 411/3

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Query Match             3.6%;  Score 137; DB 2; Length 616;
Best Local Similarity  20.2%;  Pred. No. 0.097;
Matches  123;  Conservative  93;  Mismatches 212;  Indels 180;  Gaps  30;
```

```
Qy     12  PGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGPGDGRPNLRMKF   71
            |:  :||      |   ::                                 | |:|:|
Db    161  GSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKA--LLNLSNGRNDTIPVLLDIAE  218

Qy      3  PG----IPGPRAEAAVGTTHPFSSPGAWLGSGSGS----GPVGAPPPS---------   42
                   |  : |     |              |                   :
Db     17  GSLSDPDQWTIF-----KDKDESEIMNPAI--LCAVRAGDKVSLLKRINDDVKVTQRLVD   69

Qy     72  QGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDNKRWRKKLIEKQ  131
                                   |   |:       |   ||:             :|
Db    219  RTGN----------------MREFINSPF---RDIYYRGQTALHIAERRCKHYVELLV--  258

Qy     43  --PGLPPSWAAMMAALYPSTDLSGCASSSSL----------------------------   70
              ||:                |: | |  | :|
Db     70  NQQNSILHIAAALGHVHIVEFIISTPNLLQNVNLMGETTLHVAARAGSLNIVEILVRFI  129

Qy    132  PQSKPAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKK---RLTDEEFREP  188
                                        |  :| |   : : :|
Db    259  ------------------AQGAD--VHAQARGR-----------FFQPKDEGGYFY---  283

Qy     71  PSSPSSSSPNEVMALK--------DVREVKENTLNEKL-FLLACDKGDYMVKKILEEN  121
                  |: :               :|  |:    :    |  :   :    |
Db    130  TESSSSYDAFIAAKSKNGDTALHAALKGKHVEVAFCLVSVKGHDVSFDKNNDEASPLYMAVE  189

Qy    189  STGK----TCLP---KALLNLSNGRNDTIPVLLD-----IAERTGNMREFINSPRRDIY  235
            | |     |  |     |: : | ||:    :||       :         | ::  |:
Db    284  --FGELPLSLAACTNQPHIVNLTE------NPHKKADMR------RQD---SRG  321

Qy    122  SSGDLNINCVDVLGRNAVTITIENENLDILQLLLDYGCQKLMERIQNPE--YSTTMDV-  177
                |:|                          || | :  ::      | :
Db    190  AGYHELVLKMLESSSSPSILASMFSGKSVIHAAMKANRDILGIVLRQDPGLIELRNEEG  249

Qy    236  YRGQTALHIAERRCKHYVELLVAQGADV---HA-QARGRFFQPKDEGGYYFGELPLSL  291
                                          |    |  |   |  ||:|:       :
Db    322  NTVLHALVAIADNTRENTKFVTKMYDLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGI  381

Qy    178  --APVILAAHRNNYEILTMLLKQDVSLPKPHAVGCECTLCSAKNKKDSLRHSRPFLDI  233
              ||  |    | |:                  |            | : : :   :|:
Db    279  ARQCKMFAKDLLAQAR--NSRELEVILNHTSSDEPLDKRGLLEERMNLSRLKLAIKYN--  334

Qy    292  AACTNQPHIVNLTENPHKKADMRRQDSRGNTVLHALVAIAD------------NTRENT  339
                |  || :|           |  ||   |  | :|:
Db    250  RTCLS--YGASMGCYEGIRYILAEFD----KAA------SSLCYVADDDGFTPIHMAAKEG  298

Qy    234  YRCLASPALIMLTEEDP---------ILRAFELSADLKELSLVEVEFRNDYEEL  278
                    | :::               | | : |||  ||:| |:| :|::: |
Db    382  KIGIFQHIIR------REVTDEDTRH----LSRKFKDWAY----GPVYSSLYDLSS-  423

Qy    340  KFVTKMYDLLLLKCARLFPDSNLEAVLNND-----------GLSPLMMAAKTGKI  383
             ||::  |  |   ||  | : ||                 | | ::
Db    299  HVRIIKFLKHCPDSRELLNNQCQNIFHVAAIAGKSKVVKYLLKLDEGKRMNNEQDINGN  358

Qy    384  GIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVYNSKI  443
                                                     |:||||||:| | :|||::|
Db    424  ----LDTCGEEASVLEILVYNSKIENR------HEMLAVEPINELLRDKWRKFGAVSFYINVV  476

Qy    335  -------QKEFVSQSN---CQQFLNTVW---FGQMSGYRRKPTCKKIMTVLTVGIF----  377
                     |::                    ||: | :||: |
Db

Qy    444  ENRHEMLAVEPINELLRDKWRKFGAV-------SFYINVVSYLCAMVIFTL-TAYYQPLEG  496
             :    || || |:| | | |:| ||        || |:| : | ::     : : ::
Db
```

```
Db     359 TPLHLATKGHRYPIVVNMLTWNDGINLRALNNEGFTALDIAETMKDN------NAYV-LY 410
                |   |   |:  :| :|    |      |  |  |    ||         : |: :  |
Qy     477 SYLCAMVIFTLTAYYQP-------LEGTPPYPYRTTVDYLRLAGEV---ITLFTGVLF 524
                |: ::|: : :   |          |:.|:.|.|.  : :||.   :|:
Db     411 KRLIWMALVSAGAPHGPNLIPLTVSQSSKQSPERYKDSVNTLMVTATLVATVTFAAGL-- 468

Qy     525 FFTNIKDLFMKKCP--GVNSLFIDGSFQLLYFIYSVLVIVSAALYLAGI-----EAYLAV 577
                | |  : :|: :.|    |.:|: :  | : :  | |     |   |      : |  |
Db     469 ---TLPGGYMSSAPHLGMAALVNKLNFKVFLLNNIAMCTSVVTVMALIWAQLGDALLTK 525

Qy     578 MVFALVLGWMNALYFTRGLKLTGTYSIMIQKI-----LFKDL-----------FRFLLVY 621
                |   | |    |  |     | |||       ::| :|            ||:
Db     526 KAFRLAL--------PLLLTAVVSMMMASVAGLTLVVSDLPWLSHLVLAIDSAFLVFL 575

Qy     622 LLFMIGYA 629
                :| :| | |:
Db     576 MLLIIPYA 583
```

Search completed: May  4, 2005, 22:15:47
Job time : 25 secs

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```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:      May  4, 2005, 22:04:33 ; Search time 83 Seconds
                                     (without alignments)
                                     4577.865 Million cell updates/sec

Title:         US-10-090-215-12
Perfect score: 3858
Sequence:    1 MADSSEGPRAGPGEVAELPG..........GQVSKESKHIWKLQSGRRRL 742

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:     1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:     1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     UniProt 03:*
               1: uniprot_sprot:*
               2: uniprot_trembl:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                         SUMMARIES
```

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3829 | 99.2 | 853 | 2 | Q86YZ6 | homo sapien |
| 2 | 3829 | 99.2 | 871 | 2 | Q8NDY7 | homo sapien |
| 3 | 3829 | 99.2 | 871 | 2 | Q96Q92 | homo sapien |
| 4 | 3829 | 99.2 | 871 | 2 | Q9HBC0 | homo sapien |
| 5 | 3828 | 99.2 | 871 | 2 | Q9HBA0 | homo sapien |
| 6 | 3695 | 95.8 | 871 | 2 | Q9EPK8 | mus musculu |
| 7 | 3693 | 95.7 | 871 | 2 | Q9ERZ8 | rattus norv |
| 8 | 3689 | 95.6 | 871 | 2 | Q9ES76 | mus musculu |
| 9 | 3681 | 95.4 | 871 | 2 | Q9EQZ4 | mus musculu |
| 10 | 3636 | 94.2 | 873 | 2 | Q9ERZ7 | mus musculu |
| 11 | 3472 | 90.0 | 803 | 2 | Q96RS7 | homo sapien |
| 12 | 3466 | 89.8 | 811 | 2 | Q8NG64 | homo sapien |
| 13 | 3389 | 87.8 | 803 | 2 | Q91XR5 | mus musculu |
| 14 | 3284 | 85.1 | 852 | 2 | Q9DFS3 | gallus gall |
| 15 | 1604.5 | 41.6 | 843 | 2 | Q8QFN9 | gallus gall |
| 16 | 1603 | 41.6 | 839 | 2 | Q6R5A3 | cavia porce |
| 17 | 1598.5 | 41.4 | 839 | 2 | Q8K1W1 | cavia porce |
| 18 | 1580.5 | 41.0 | 838 | 2 | Q9JM57 | rattus norv |
| 19 | 1580 | 41.0 | 839 | 2 | Q704Y3 | mus musculu |
| 20 | 1579.5 | 40.9 | 838 | 2 | O35433 | rattus norv |
| 21 | 1563 | 40.5 | 829 | 2 | Q68SW0 | mus musculu |
| 22 | 1557 | 40.4 | 839 | 2 | Q8NER1 | homo sapien |
| 23 | 1556.5 | 40.3 | 839 | 2 | Q9NQ74 | homo sapien |
| 24 | 1555.5 | 40.3 | 839 | 2 | Q9NY22 | homo sapien |
| 25 | 1552.5 | 40.2 | 842 | 2 | Q6RX08 | oryctolagus |
| 26 | 1551.5 | 40.2 | 839 | 2 | Q9H0G9 | homo sapien |
| 27 | 1551.5 | 40.2 | 839 | 2 | Q9H304 | homo sapien |
| 28 | 1547 | 40.1 | 840 | 2 | Q697L1 | canis famil |
| 29 | 1369 | 35.5 | 778 | 2 | Q9JM56 | rattus norv |
| 30 | 1324 | 34.3 | 761 | 2 | Q9WUD2 | rattus norv |
| 31 | 1322 | 34.3 | 761 | 2 | Q9QYH8 | rattus norv |
| 32 | 1322 | 34.3 | 762 | 2 | Q9JMI8 | rattus norv |
| 33 | 1321 | 34.2 | 791 | 2 | Q8K424 | mus musculu |
| 34 | 1316 | 34.1 | 790 | 2 | Q8NFH2 | homo sapien |
| 35 | 1312 | 34.0 | 790 | 2 | Q8NDW7 | homo sapien |
| 36 | 1309 | 33.9 | 765 | 2 | Q8NET9 | homo sapien |
| 37 | 1309 | 33.9 | 791 | 2 | Q8NET8 | homo sapien |
| 38 | 1304.5 | 33.8 | 756 | 2 | Q6JGX2 | f-11 rat/mo |
| 39 | 1304.5 | 33.8 | 756 | 2 | Q9WTR1 | mus musculu |
| 40 | 1304.5 | 33.8 | 756 | 2 | Q99K71 | mus musculu |
| 41 | 1298.5 | 33.7 | 764 | 2 | Q9Y5S1 | homo sapien |
| 42 | 1287 | 33.4 | 764 | 2 | Q9Y670 | homo sapien |
| 43 | 1071 | 27.8 | 511 | 2 | Q9H303 | homo sapien |
| 44 | 1041 | 27.0 | 468 | 2 | Q920B4 | rattus norv |
| 45 | 1007.5 | 26.1 | 528 | 2 | Q9Z182 | rattus norv |

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                              ALIGNMENTS

RESULT 1
Q86YZ6
ID   Q86YZ6;              PRELIMINARY;       PRT;     853 AA.
AC   Q86YZ6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein TRPV-SV.
GN   Name=TRPV-SV;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suzuki S.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Suzuki M.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB100308; BAC55864.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Hypothetical Protein; Ion transport; Ionic channel;
KW   Transmembrane; Transport.
SQ   SEQUENCE 853 AA;  96448 MW;  EAA0719660GAED20 CRC64;

Query Match             99.2%;  Score 3829;  DB 2;  Length 853;
Best Local Similarity   100.0%;  Pred. No. 1.4e-231;
Matches  736;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFPYGTYRHHSSDN 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMS; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   871 AA;   98280 MW;  C62056B86CSA6FB6 CRC64;
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Query Match             99.2%;  Score 3829;  DB 2;  Length 871;
Best Local Similarity  100.0%;  Pred. No. 1.4e-231;
Matches 736;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITHLFTGVLFFFTNIKDLFMKKCPGV 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITHLFTGVLFFFTNIKDLFMKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQ 736
         ||||||||||||||||
Db  721 TVGQVSKESKHIWKLQ 736
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RESULT 2
Q8NDY7
ID   Q8NDY7;        PRELIMINARY;        PRT;     871 AA.
AC   Q8NDY7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor-like channel 2.
GN   Name=VRL2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22107054; PubMed=12077606; DOI=10.1038/nature00894;
RA   Smith G.D., Gunthorpe M.J., Kelsell R.E., Hayes P.D., Reilly P.,
RA   Facer P., Wright J.B., Jerman J.C., Walhin J-P., Ooi L., Egerton J.,
RA   Charles K.J., Smart D., Randall A.D., Anand P., Davis J.B.;
RT   "TRPV3 is a temperature-sensitive vanilloid receptor-like protein.";
RL   Nature 418:186-190(2002).
DR   EMBL; AJ296305; CAC82937.1; -.
DR   Genew; HGNC:18083; TRPV4.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
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Db    721 TVGQVSKESKHIWKLQ 736
          ||||||||||||||||
Qy    721 TVGQVSKESKHIWKLQ 736

RESULT 3
Q96Q92
ID   Q96Q92              PRELIMINARY;      PRT;   871 AA.
AC   Q96Q92;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor like channel-2.
GN   Name=VRL-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ishibashi K.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB032427; BAB69040.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF00023; Ank; 3.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   871 AA;  98266 MW;  C62056A401ECABB6 CRC64;

Query Match             99.2%;  Score 3829;  DB 2;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 1.4e-231;
Matches  736;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60

Qy     61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120

Qy    121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180

Qy    181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy    241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI 300

Qy    301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
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Qy    361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy    421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy    481 AMVIFTLTAYYQPLEGTPYPYRTTVDYLRLAGVITLFTGVLFFFTNIKDLFMKKCPGV 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AMVIFTLTAYYQPLEGTPYPYRTTVDYLRLAGVITLFTGVLFFFTNIKDLFMKKCPGV 540

Qy    541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy    601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660

Qy    661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720

Qy    721 TVGQVSKESKHIWKLQ 736
          ||||||||||||||||
Db    721 TVGQVSKESKHIWKLQ 736

RESULT 4
Q9HBC0
ID   Q9HBC0              PRELIMINARY;      PRT;   871 AA.
AC   Q9HBC0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   OTRPC4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Renal cortex;
RX   MEDLINE=20482174; PubMed=11025659; DOI=10.1038/35036318;
RA   Strotmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;
RT   "OTRPC4, a nonselective cation channel that confers sensitivity to
RT   extracellular osmolarity.";
RL   Nat. Cell Biol. 2:695-702(2000).
DR   EMBL; AF258465; AAG16127.1; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0015281; F:nonselective cation channel activity; NAS.
DR   GO; GO:0006816; P:calcium ion transport; NAS.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE   871 AA;  98294 MW;  C62055B86DEA6FB6 CRC64;

Query Match             99.2%;  Score 3829;  DB 2;  Length 871;
Best Local Similarity   100.0%;  Pred. No. 1.4e-231;
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Matches  736;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480

Qy  481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV   540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV   540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600

Qy  601 TYSIMIQKILFKDLFRFLLVILLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVILLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660

Qy  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIIILTFVLLLNMLIALMGE        720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIIILTFVLLLNMLIALMGE        720

Qy  721 TVGQVSKESKHIWKLQ  736
        ||||||||||||||||
Db  721 TVGQVSKESKHIWKLQ  736
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RESULT 5
Q9HBA0

ID   Q9HBA0
AC   Q9HBA0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor-related osmotically activated channel.
GN   Name=VROAC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20531888; PubMed=11081638; DOI=10.1016/S0092-8674(00)00143-4;
RA   Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA   Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
RT   "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT   candidate vertebrate osmoreceptor.";
RL   Cell 103:525-535 (2000).
DR   EMBL; AF263523; AAG28029.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   871 AA;  98265 MW;  A86FB6ECC9103C19 CRC64;

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Query Match             99.2%;  Score 3828;  DB 2;  Length 871;
Best Local Similarity   99.9%;  Pred. No. 1.6e-231;
Matches  735;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP   60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420
        ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db  361 NLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD  420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480

Qy  481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV   540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV   540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600

Qy  601 TYSIMIQKILFKDLFRFLLVILLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
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Db  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
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Qy  661 RDSETFSTFLLDLFKLITGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
        ||||||||||||||||
Db  661 RDSETFSTFLLDLFKLITGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
Qy  721 TVGQVSKESKHIWKLQ 736
        ||||||||||
Db  721 TVGQVSKESKHIWKLQ 736
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RESULT 6
Q9EPK8
ID   Q9EPK8      PRELIMINARY;     PRT;   871 AA.
AC   Q9EPK8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Transient receptor potential protein 12.
GN   Name=Trpv4; Synonyms=Trp12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=20547522; PubMed=11094154; DOI=10.1016/S0014-5793(00)02212-2;
RA   Wissenbach U., Boeding M., Freichel M., Flockerzi V.;
RT   "Trp12, a novel Trp related protein from kidney.";
RL   FEBS Lett. 485:127-134(2000).
DR   EMBL; AJ296078; CAC20703.1; -.
DR   MGD; MGI:1926945; Trpv4.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005262; F:calcium channel activity; IDA.
DR   GO; GO:0005034; F:osmosensor activity; IDA.
DR   GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR   GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR   GO; GO:0044484; P:regulation of response to osmotic stress; IMP.
DR   GO; GO:0030103; P:vasopressin secretion; IMP.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   871 AA;  98026 MW;  5BAC6E33F89CEA05 CRC64;

Query Match             95.8%;  Score 3695;  DB 2;  Length 871;
Best Local Similarity   95.7%;  Pred. No. 3.5e-223;
Matches  704;  Conservative  16;  Mismatches  16;  Indels  0;  Gaps  0;

Qy    1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
        |||  |||||| |||| ||||||||  ||||||||||||||||:|||:|||:|||||||||
Db    1 MADPGDGPRAAPGEVAEPPGDESGTSCGGEAFPLSSLANLFEGEEGSSSLSPVDASRPAGP 60

Qy   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
        |||||||||||||||||||||||||||||||| :||||||||||||||||||||||| ||
Db   61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYSSSVVPGPKKAPMDSLFDYGTYRHPSDN 120

Qy  121 KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLLDGLLPFLLTHKKRL 180
        ||||||  ::|:||||:||||||||||||||| |||||||:||||| |||||:||:|||||
Db  121 KRWRKKVVEKQPQSPKAPAPQPPPILKVFNRPLFDIVSRGSTADLDGLLSFLLTHKKRL 180
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Qy  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy  241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300
        :||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 SLHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI 300

Qy  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
        |||||||||||||||||||||||||||||||||||||||||||||||:|||||||:|||||
Db  301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCSRLFPDS 360

Qy  361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
        |||:||||||||||||||||||:|||:|||||||||||||||:||||||||||||||||
Db  361 NLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy  421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
        ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LSSLDTCGEEVSVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
        |||||||||||||||||||||||||||||||||||||||||||:::||||:|||||||
Db  481 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTSIKDLFTKKCPGV 540

Qy  541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
        |||||:||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db  541 NSLFVDGSFQLLYFIYSVLVVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
        ||||||||||||||||||||||||||||||||||||||:|||||:||:|||||||||||
Db  601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCTNMKVCDEDQSNCTVPTYPAC 660

Qy  661 RDSETFSTFLLDLFKLITGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720
        ||||||:||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db  661 RDSETFSAFLLDLFKLITGMGDLEMLSSAKYPVVFIILLVTYIILTFVLLLNMLIALMGE 720

Qy  721 TVGQVSKESKHIWKLQ 736
        ||||||||||||||||
Db  721 TVGQVSKESKHIWKLQ 736
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RESULT 7
Q9ER28
ID   Q9ER28      PRELIMINARY;     PRT;   871 AA.
AC   Q9ER28;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor-related osmotically activated channel.
GN   Name=Vroac;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=kidney;
RX   MEDLINE=20531888; PubMed=11081638; DOI=10.1016/S0092-8674(00)00143-4;
RA   Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA   Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
RT   "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT   candidate vertebrate osmoreceptor.";
RL   Cell 103:525-535(2000).
DR   EMBL; AF263521; AAG28027.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
```

DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00520; Ank; 3.
DR   Pfam; PF00023; Ion_trans; 1.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   871 AA;  98009 MW;  5D50684DA08C354B CRC64;

Query Match             95.7%;  Score 3693;  DB 2;  Length 871;
Best Local Similarity   95.5%;  Pred. No. 4.7e-223;
Matches  703;  Conservative   16;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60
           |||  ||| ||| ||: ||||||| |||||||||||||||||| :|| ||| ||||||||
Db      1  MADPGDGPRAAPGDVAEPPGDESGTSGGEAFPLSSLANLFEGEGGSSSLSPVDASRPAGP  60

Qy     61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db     61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHPSDN 120

Qy    121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
           ||||:|::|||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    121  KRWRRKVVEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLSFLLTHKKRL 180

Qy    181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy    241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300

Qy    301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db    301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCSRLFPDS 360

Qy    361  NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
           |||:||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db    361  NLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy    421  LSSLDTCGEEASVLEILIVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLC 480
           ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  LSSLDTCGEEVSVLEILIVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLC 480

Qy    481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
           ||||||||||||||||||||||||||||||||||||||:||||||||:||||||||||||
Db    481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLLTGVLFFFTSIKDLFMKKCPGV 540

Qy    541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
           ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  NSLFVDGSFQLLYFIYSVLVVVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy    601  TYSIMIQKILFKDLFRFLLVVLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
           ||||||||||||||||||||||||||||||||||||||||:|||||||||:|||||:||:|
Db    601  TYSIMIQKILFKDLFRFLLVVLLFMIGYASALVSLLNPCTNMKVCNEDQSNCTVPSYPAC 660

Qy    661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFILLVTYIILTFVLLNMLIALMGE  720
           |||||||:|||||||||||||||||||||:|||||||||||||||||||||||||||||
Db    661  RDSETFSAFLLDLFKLTIGMGDLEMLSSAKYPVVFILLVTYIILTFVLLNMLIALMGE  720

Qy    721  TVGQVSKESKHIWKLQ 736
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Db    721  TVGQVSKESKHIWKLQ 736

ID   Q9ES76                  PRELIMINARY;      PRT;   871 AA.
AC   Q9ES76;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   OTRPC4 cation channel.
GN   Name=Trpv4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvEv;
RX   MEDLINE=20481174; PubMed=11025659; DOI=10.1038/35036318;
RA   Strotmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;
RT   "OTRPC4, a nonselective cation channel that confers sensitivity to
RT   extracellular osmolarity.";
RL   Nat. Cell Biol. 2:695-702(2000).
DR   EMBL; AF209026; AAG17543.1; -.
DR   MGD; MGI:1926945; Trpv4.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005262; F:calcium channel activity; IDA.
DR   GO; GO:0005034; F:osmosensor activity; IDA.
DR   GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR   GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR   GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR   GO; GO:0030103; P:vasopressin secretion; IMP.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE   871 AA;  98069 MW;  2B22BD54083F00A CRC64;

Query Match             95.6%;  Score 3689;  DB 2;  Length 871;
Best Local Similarity   95.5%;  Pred. No. 8.4e-223;
Matches  703;  Conservative   16;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP  60
           |||  ||| ||| ||: ||||||| |||||||||||||||||| :|| ||| ||||||||
Db      1  MADPGDGPRAAPGDVAEPPGDESGTSGGEAFPLSSLANLFEGEGGSSSLSPVDASRPAGP  60

Qy     61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db     61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHPSDN 120

Qy    121  KRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
           ||||:|::|||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    121  KRWRRKVVEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLSFLLTHKKRL 180

Qy    181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy    241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  SLHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYYFGELPLSLAACTNQPHI  300

Qy    301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db    301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCCSRLFPDS 360

RESULT 8
Q9ES76

Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
        |||:|||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db 361 NLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
        ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 LSSLDTCGEEVSVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
        |||||||||||||||||||||||||||||||||||||||||||||:|||||:|||||||
Db 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLFFFTSIKDLFTKKCPGV 540

Qy 541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
        ||||:|||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db 541 NSLFVDGSFQLLYFIYSVLVVVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy 601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
        |||||||||||||||||||||||||||||||||:||||:||||||:||:|||||||||:|
Db 601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVTLLNPCTNMKVCDEDQSNCTVPTYPAC 660

Qy 661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
        |||||||:||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db 661 RDSETFSAFLLDLFKLTIGMGDLEMLSSAKYPVVFIILLVTYIILTFVLLNMLIALMGE 720

Qy 721 TVGQVSKESKHIWKLQ 736
        ||||||||||||||||
Db 721 TVGQVSKESKHIWKLQ 736

RESULT 9
Q9EQ24
ID   Q9EQ24                  PRELIMINARY;   PRT;   871 AA.
AC   Q9EQ24;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ion channel.
GN   Name=Trpv4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22692536; PubMed=12692122; DOI=10.1074/jbc.M302561200;
RA   Suzuki M., Mizuno A., Kodaira K., Imai M.;
RT   "Impaired pressure sensation in mice lacking TRPV4.";
RL   J. Biol. Chem. 278:22664-22668(2003).
DR   EMBL; AB021875; BAA83731.2; -.
DR   MGD; MGI:1926945; Trpv4;
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005262; F:calcium channel activity; IDA.
DR   GO; GO:0005034; F:osmosensor activity; IDA.
DR   GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR   GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR   GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR   GO; GO:0030103; P:vasopressin secretion; IMP.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.

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SQ   SEQUENCE   871 AA;   98060 MW;   3285AE576D32DD95 CRC64;

        Query Match              95.4%;  Score 3681;  DB 2;  Length 871;
        Best Local Similarity    95.2%;  Pred. No. 2.7e-222;
        Matches 701;  Conservative 17;  Mismatches 18;  Indels 0;  Gaps 0;

Qy   1 MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGP 60
        |||  |||:|||||||| ||||||| :||||||||||||||||||:|| |||| ||||||
Db   1 MADPDGDPRAAPGEVAEPPGDESGTSGGEAFPLSSLANLFEGEGGSSLSPVDASRPAGP 60

Qy  61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db  61 GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHPSDN 120

Qy 121 KRWRKKIIEKQPOSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRL 180
        ||||:|::|||| |||:|||||| ||||||||||||||||||||||||||||:||||||
Db 121 KRWRRKVVEKQPQSPKTPAPQPPILKVFNRPILFDIVSRGSTADLDGLLSFLLTHKKRL 180

Qy 181 TDEEFRRPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT 240
        ||||||||||||||||||||||||||||:| ||||||||||||||||||||||||||||
Db 181 TDEEFRRPSTGKTCLPKALLNLSNGRNDTLQVLLDIAERTGNMREFINSPFRDIYYRGQT 240

Qy 241 ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYGELPLSLAACTNQPHI 300
        :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 SLHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYGELPLSLAACTNQPHI 300

Qy 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db 301 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCSRLFPDS 360

Qy 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420
        |||:|||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db 361 NLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420

Qy 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
        ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 LSSLDTCGEEVSVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Qy 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV 540
        |||||||||||||||||||||||||||||||||||||||||||||:|||||:|||||||
Db 481 AMVIFTLTAYYQPLEGTPPYRTTVDYLRLAGEVITLFTGVLFFFTSIKDLFTKKCPGV 540

Qy 541 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600
        ||||:|||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db 541 NSLFVDGSFQLLYFIYSVLVVVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG 600

Qy 601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC 660
        |||||||||||||||||||||||||||||||||:||||:||||||:||:|||||||||:|
Db 601 TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVTLLNPCTNMKVCDEDQSNCTVPTYPAC 660

Qy 661 RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLNMLIALMGE 720
        |||||||:||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db 661 RDSETFSAFLLDLFKLTIGMGDLEMLSSAKYPVVFIILLVTYIILTFVLLNMLIALMGE 720

Qy 721 TVGQVSKESKHIWKLQ 736
        ||||||||||||||||
Db 721 TVGQVSKESKHIWKLQ 736

RESULT 10
Q9ERZ7
ID   Q9ERZ7                  PRELIMINARY;   PRT;   873 AA.
AC   Q9ERZ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor-related osmotically activated channel.
GN   Name=Trpv4; Synonyms=Vroac;
OS   Mus musculus (Mouse);
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Hypothalamus;
RX   MEDLINE=20531888; PubMed=11081638; DOI=10.1016/S0092-8674(00)00143-4;
RA   Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA   Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
RT   "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT   candidate vertebrate osmoreceptor.";
RL   Cell 103:525-535(2000).
DR   EMBL; AF263522; AAG28028.1; -.
DR   MGD; MGI:1926945; Trpv4.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005262; F:calcium channel activity; IDA.
DR   GO; GO:0005034; F:osmosensor activity; IDA.
DR   GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR   GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR   GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR   GO; GO:0030103; P:vasopressin secretion; IMP.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   873 AA;  98596 MW;  5DD87C92712B24EA CRC64;

Query Match             94.2%;  Score 3636;  DB 2;  Length 873;
Best Local Similarity   94.4%;  Pred. No. 1.8e-219;
Matches  697;  Conservative   17;  Mismatches   22;  Indels    2;  Gaps    2;

Qy    1  MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPA-DASRPAG   59
         ||| |.|||| ||||||.||||||.||||||||||||||||||||.|. .||  :.||||
Db    1  MADPGDGPRAAPGEVAEPPGDESGTSGGEAFPLSSLANLFEGEESSYFSYPRWTASRPAG   60

Qy   60  PGDGRPNLRMKF-QGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSS  118
         ||||||||||||  |:|||||||||||||||||||||||||||||||||||||||||| |
Db   61  PGDGRPNLRMKFGRSAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHPS  120

Qy  119  DNKRWRKKIIEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKK  178
         |||||| |:|:||||||||||||||||||||||||||||||||||||||||||.||||||
Db  121  DNKRWRRKVVEKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLSFLLTHKK  180

Qy  179  RLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRG  238
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  RLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRG  240

Qy  239  QTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQP  298
         ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  QTSLHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQP  300

Qy  299  HIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFP  358
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||.|||
Db  301  HIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCSRLFP  360

Qy  359  DSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSL  418
         |||||.|||||||||||||||||||||.||||||||||||||||||||||||||||||||
Db  361  DSNLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSL  420

Qy  419  YDLSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSY  478
         ||||||||||||.|||||||.|||||||||||||||||||||||||||||||||||||.|
Db  421  YDLSSLDTCGEEVSVLEILVVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVPY  480

Qy  479  LCAMVIFLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCP  538
         ||||||| |||||||||||||||||||||||||||||||||||||||| :||||| ||||
Db  481  LCAMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTSIKDLFTKKCP  540

Qy  539  GVNSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKL  598
         ||||||.||||||||||||||||.||||||||||||||||||||||||||||||||||||
Db  541  GVNSLFVDGSFQLLYFIYSVLVVVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKL  600

Qy  599  TGTYSIMIQKILFKDLFRFLLVYLLFMIGYASAIVSLLNPCANMKVCNEDQTNCTVPTYP  658
         |||||||||||||||||||||||||||||||||::.|||||:|||||:|||:|||||||||
Db  601  TGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALVTLLNPCTNMKVCDEDQSNCTVPTYP  660

Qy  659  SCRDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFILLLVTYIILTFVLLLNMLIALM  718
         :|||||||:||||||||||||||||||||||:||||||||||||||||||||||||||||
Db  661  ACRDSETFSAFLLDLFKLTIGMGDLEMLSSAKYPVVFILLLVTYIILTFVLLLNMLIALM  720

Qy  719  GETVGQVSKESKHIWKLQ  736
         ||||||||||||||||||
Db  721  GETVGQVSKESKHIWKLQ  738
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RESULT 11
Q96RS7
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ID   Q96RS7        PRELIMINARY;       PRT;   803 AA.
AC   Q96RS7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor-like protein 2.
GN   Name=VRL2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Derst C., Schafer M.K.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF279673; AAK69487.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   803 AA;  91635 MW;  AB329C595B325784 CRC64;

Query Match             90.0%;  Score 3472;  DB 2;  Length 803;
Best Local Similarity  100.0%;  Pred. No. 3.1e-209;
Matches  668;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   69  MKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDNKRWRKKII  128
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDNKRWRKKII   60

Qy  129  EKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREP  188
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  EKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREP  120
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DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ   SEQUENCE   811 AA;  91220 MW;  3847D0FD07830781 CRC64;

     Query Match            89.8%;   Score 3466;   DB 2;   Length 811;
     Best Local Similarity  91.6%;   Pred. No. 7.5e-209;
     Matches  674;   Conservative   0;   Mismatches   2;   Indels   60;   Gaps   1;

Qy     1  MADSSEGPRAGPGEVAELPGDESGTPGGEAPLSSLANLFEGEDGSLSPSPADASRPAGP  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MADSSEGPRAGPGEVAELPGDESGTPGGEAPLSSLANLFEGEDGSLSPSPADASRPAGP  60

Qy    61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GDGRPNLRMKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDN  120

Qy   121  KRWRKKIIEKQPQSPKAPAPQPPPILKVNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  KRWRKKIIEKQPQSPKAPAPQPPPILKVNRPILFDIVSRGSTADLDGLLPFLLTHKKRL  180

Qy   181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQT  240

Qy   241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHI  300

Qy   301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS  360

Qy   361  NLEAVLNNDGLSPLMMAAKTGKIG------------------------------------  384
          ||||||||||||||||||||||||
Db   361  NLEAVLNNDGLSPLMMAAKTGKIG  385

Qy   421  LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385  ---------------------------NRHEMLAAEPINELLRDKWRKFGAVSFYINVSYLC  420

Qy   481  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGV  480

Qy   541  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG  540

Qy   601  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSC  600

Qy   661  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  RDSETFSTFLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGE  660

Qy   721  TVGQVSKESKHIWKLQ  736
          ||||||||||||||||
Db   661  TVGQVSKESKHIWKLQ  676
```

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RESULT 13
Q91XR5
ID   Q91XR5;                   PRELIMINARY;        PRT;   803 AA.
AC   Q91XR5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor-like protein 2.
GN   Name=Trpv4; Synonyms=Vrl2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Left column (RESULT 12):

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Qy   189  STGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIER  248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  STGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIER  180

Qy   249  RCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENP  308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  RCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENP  240

Qy   309  HKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNN  368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  HKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNN  300

Qy   369  DGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCG  428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  DGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCG  360

Qy   429  EEASVLEILVLVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT  488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  EEASVLEILVLVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT  420

Qy   489  AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGS  548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGS  480

Qy   549  FQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQK  608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  FQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQK  540

Qy   609  ILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSCRDSETFST  668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  ILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSCRDSETFST  600

Qy   669  FLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKE  728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  FLLDLFKLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKE  660

Qy   729  SKHIWKLQ  736
          ||||||||
Db   661  SKHIWKLQ  668
```

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RESULT 12
Q8NG64
ID   Q8NG64;                   PRELIMINARY;        PRT;   811 AA.
AC   Q8NG64;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   OTRPC4beta cation channel.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aortic endothelium;
RA   Xu F., Satoh E., Iijima T.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB073669; BAC06573.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
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OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Derst C., Schafer M.K.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF279672; AAK69486.1; -.
DR   MGD; MGI:1926945; Trpv4.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005262; F:calcium channel activity; IDA.
DR   GO; GO:0005034; F:osmosensor activity; IDA.
DR   GO; GO:0042538; P:hyperosmotic salinity response; IMP.
DR   GO; GO:0007231; P:osmosensory signaling pathway; IDA.
DR   GO; GO:0047484; P:regulation of response to osmotic stress; IMP.
DR   GO; GO:0030103; P:vasopressin secretion; IMP.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   803 AA;   91438 MW;   79A5BD9323300029 CRC64;

Query Match             87.8%;  Score 3389; DB 2; Length 803;
Best Local Similarity   96.6%;  Pred. No. 5e-204;
Matches  645; Conservative  14; Mismatches  9; Indels  0; Gaps  0;

Qy    69  MKFQGAFRKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDNKRWRKKII  128
          |||||||||||||||||||||||||||||||||||||||||||||||||:||:|:||
Db     1  MKFQGAFRKGVPNPIDLLESTRYESSVVPGPKKAPMDSLFDYGTYRHHPSDNKRWRRRKVV   60

Qy   129  EKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREP  188
          |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db    61  EKQPQSPKAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLSFLLTHKKRLTDEEFREP  120

Qy   189  STGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIER  248
          |||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db   121  STGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQTSLHIAIER  180

Qy   249  RCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENP  308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  RCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENP  240

Qy   309  HKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLRAVLNN  368
          |||||||||||||||||||||||||||||||||||||||||||:||||||:|||||||||
Db   241  HKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCSRLFPDSNLETVLNN  300

Qy   369  DGLSPLMMAAKTGKIGLFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCG  428
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  DGLSPLMMAAKTGKIGVFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCG  360

Qy   429  EEASVLEILVVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT  488
          ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  EEVSVLEILVVNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT  420

Qy   489  AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGS  548
          ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db   421  AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTSIKDLFYKKCPGVNSLFVDGS  480

Qy   549  FQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQK  608
          ||||||||||||::|||||||||||:||||||||||||||||||||||||||||||||||
Db   481  FQLLYFIYSVLVVVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQK  540

Qy   609  ILFKDLFRFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSCRDSETFST  668
          ||||||||||||||||||||||||||:|||||:|||||||||:|||||||:||||||||
Db   541  ILFKDLFRFLLVYLLFMIGYASALVTLLNPCTNMKVCDEDQSNCTVPTYPACRDSETFSA  600
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Qy   669  FLLDLFKLTIGMGDLEMLSSTKYPVVFILLVVYIILTFVLLLNMLIALMGETVGQVSKE  728
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   601  FLLDLFKLTIGMGDLEMLSSAKYPVVFILLVVYIILTFVLLLNMLIALMGETVGQVSKE  660

Qy   729  SKHIWKLQ  736
          ||||||||
Db   661  SKHIWKLQ  668

RESULT 14
Q9DFS3
ID   Q9DFS3          PRELIMINARY;    PRT;   852 AA.
AC   Q9DFS3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor-related osmotically activated channel protein.
GN   Name=VR-OAC;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cochlea;
RX   MEDLINE=20531888; PubMed=11081638; DOI=10.1016/S0092-8674(00)00143-4;
RA   Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S., Sali A.,
RA   Hudspeth A.J., Friedman J.M., Heller S.;
RT   "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT   candidate vertebrate osmoreceptor.";
RL   Cell 103:525-535(2000).
DR   EMBL; AF261883; AAG28026.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR002016; Peroxidase.
DR   InterPro; IPR001865; Ribosomal_S2.
DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vanil_receptor.
DR   InterPro; IPR008348; Vanil_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 3.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1.
DR   PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   852 AA;   96197 MW;   E85365D3FADD08C1 CRC64;

Query Match             85.1%;  Score 3284; DB 2; Length 852;
Best Local Similarity   86.5%;  Pred. No. 2.1e-197;
Matches  624; Conservative  43; Mismatches  50; Indels  4; Gaps  2;

Qy    17  ELPGDRSGTPGGEAFPLSSLANLFEGEDGSLSPSPADASR-PAGPGDGRPNLRMKFQGAF   75
          :|||  ::||:|| ||:|||||:||||||:|||:||:||  :||:|||:||||:||
Db     5  EDPRDAGDVLGDDSFPLSSLANLFEVED---TPSPAPSRGPGPGAGDGKQNLRMKFHGAF   61

Qy    76  RKGVPNPIDLLESTLYESSVVPGPKKAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSP  135
          |||||||||||||||||||||||||||||||||||||||||::::||
Db    62  RKGPPKPMELLESTIYESSVVPAPKKAPMDSLFDYGTYRQHPSENKRWRRRVEKPVAGT  121

Qy   136  KAPAPQPPPILKVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCL  195
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DR   InterPro; IPR004729; TRPChannel.
DR   InterPro; IPR008347; Vani1_receptor.
DR   InterPro; IPR008348; Vani1_receptor2.
DR   Pfam; PF00023; Ank; 3.
DR   Pfam; PF00520; Ion_trans; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PRINTS; PR01768; TRPVRECEPTOR.
DR   PRINTS; PR01769; VRL2RECEPTOR.
DR   SMART; SM00248; ANK; 4.
DR   TIGRFAMs; TIGR00870; trp; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
KW   ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW   Transport.
SQ   SEQUENCE   843 AA;  96520 MW;  ABB3592C9DC179C8 CRC64;

Query Match             41.6%;  Score 1604.5;  DB 2;  Length 843;
Best Local Similarity   47.5%;  Pred. No. 4.7e-92;
Matches  343;  Conservative  128;  Mismatches  184;  Indels  67;  Gaps  18;

Qy   41  EGEDGSLSPSPADASRPAGPGDGRPNLRMKFQGAFRKGVPNPIDLLESTLY--ESSVVPG  98
Db   27  DGEDSAL--ETAD------------------------NLQGTF----SNKVQPSKSNIFARRGRFVMG  64

Qy   99  ---PKKAPMDSLFDY------GTYRHSSDNKRWRKKIIEKQP---QSPKAPAPQPPPIL  146
Db   65  DCDKDMAPMDSFYQMDHLMAPSVIKFHANMERGKLHKLLSTDSITGCSEKA--------F  116

Qy  147  KVFNRPILFDIVSRGSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGR  206
Db  117  KFYDRRRIFDAVARGSTKDLDDILLLYLNRTLKHLTDDEFKEPETGKTCLLKAMLNLHDGK  176

Qy  207  NDTIPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHA  266
Db  177  NDTIPLLLDIAKKTGTLKEFVNAEYTDNYKGQTALHIAIERRNMYLVKLLVQNGADVHA  236

Qy  267  QARGRFFQP-KDEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVL  325
Db  237  RACGEFFRKIKGKPG--FYFGELPLSLAACTNQLCIVKFLLENPYQAADIAAEDSMGNMVL  295

Qy  326  HALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGI  385
Db  296  HTLVEIADNTKDNTKFVTKMYNNLILGAKINPILKLEELTNKKGLTPLTLAAKTGKIGI  355

Qy  386  FQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVNSKIEN  445
Db  356  FAYILRREIKDPECRHLSRKFTEWAYGPVHSSLYDLSCIDTC-EKNSVEIIAYSSETPN  414

Qy  446  RHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLTAYYQPLE--GTPPYPY-  502
Db  415  RHEMLLVEPLNRLLQDKWDRFVCHLFYFNFFVAIHISLTTAYYRPVQKGDKPPFAFG  474

Qy  503  RTTVDYLRLAGEVITLFTGVLFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIV  562
Db  475  HSTGEYFRVTGEILSVLGGLYFFRGIQ-YFVQRRPSLKTLIVDSYSEVLFFVHSLLLLS  533

Qy  563  SAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRPLLVYL  622
Db  534  SVVLYFCCGQELYVASMVFSLALGWANMLYYTRGFQQMGIYSVMIAKMILRDLCRFMFVYL  593

Qy  623  LFMIGYASALVSLLNPCANMKVCNEDQ-TNCTVPTYPSCRDSETFST------FLLDLF  674
Db  594  VFLLGFSTAVTVLIED------DNEGQDTNSS--EYARCSHTKGRTSYNSLYYTCLELF  645

Qy  675  KLTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWK  734
Db  646  KFTIGMGDLEFTENYRFKSVFVILLLVLVVILTYILILLNMLIALMGETVSKIAQESKSIWK  705

Qy  735  LQ  736
Db  706  LQ  707
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RESULT 15
Q8QFN9
ID   Q8QFN9        PRELIMINARY;      PRT;   843 AA.
AC   Q8QFN9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vanilloid receptor-like protein.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dorsal root ganglia;
RX   MEDLINE=21842900; PubMed=11853675; DOI=10.1016/S0092-8674(02)00637-2;
RA   Jordt S.E., Julius D.;
RT   "Molecular basis for species-specific sensitivity to 'hot' chili
RT   peppers.";
RL   Cell 108:421-430(2002).
DR   EMBL; AY072909; AAL78069.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005261; F:cation channel activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
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Db  122  KGPAPNPPVLKVFNRPILFDIVSRGSPDGLEGLLSFLLTHKKRLTDEEFREPSTGKTCL  181
Qy  196  PKALLNLSNGRNDTIPVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVE  255
Db  182  PKALLNLSAGRNDTIPILLDIAEKTGNMREFINSPFRDVYYRGQTALHIAIERRCKHYVE  241

Qy  256  LLIVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMR  315
Db  242  LLIVEKGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACTNQPHIVHYLTENGHKQADLR  301

Qy  316  RQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLM  375
Db  302  RQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCAKLFPDTNLEALLNNDGLSPLM  361

Qy  376  MAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLE  435
Db  362  MAAKTGKIGIFQHIIRREIADDDVRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEVSVLE  421

Qy  436  ILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLIAYYRPME  495
Db  422  ILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYISVVSYLCAMIIFTLIAYYRPME  481

Qy  496  GTPPYPYRTTVDYLRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQLLYFI  555
Db  482  GPPPYPYTTTIDYLRLAGEIITLLTGLLFFFSNIKDLFMKKCPGVNSFFIDGSFQLLYFI  541

Qy  556  YSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLF  615
Db  542  YSVLVIVTAGLYLGGVEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLF  601

Qy  616  RFLLVYLLFMIGYASALVSLLNPCANMKVCNEDQTNCTVPTYPSCRDSETFSTFLLDLFK  675
Db  602  RFLLVYLLFMIGYASALVSLLNPCPSSESCSEDHSNCTLPTYPSCRDSQTFSTFLLDLFK  661

Qy  676  LTIGMGDLEMLSSTKYPVVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKL  735
Db  662  LTIGMGDLEMLESAKYPGVFIILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKL  721

Qy  736  Q  736
Db  722  Q  722
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